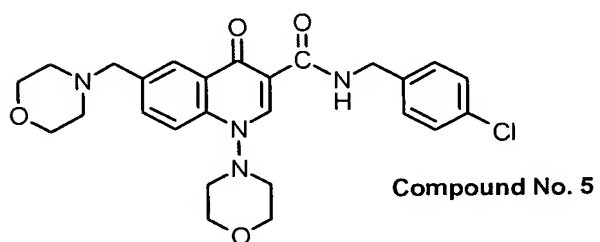
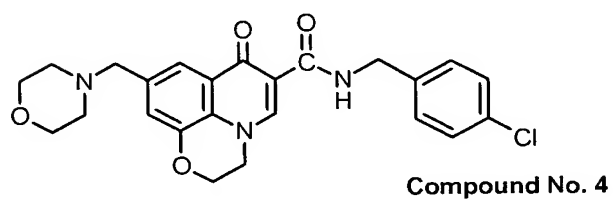
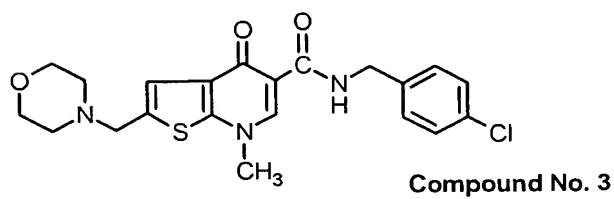
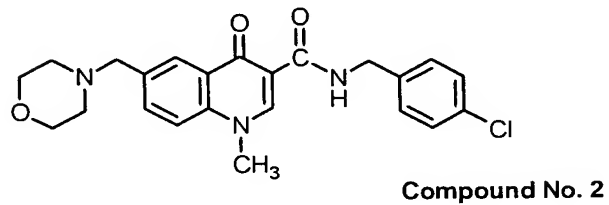
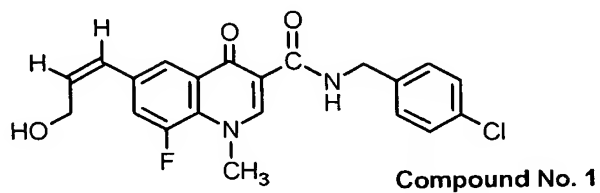
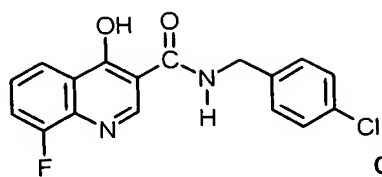
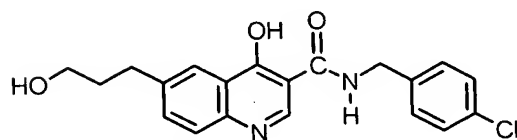


**Figure 1**      **4-HQ, 4-oxo-DHQ and 4-oxo-DHTP antiviral compounds**

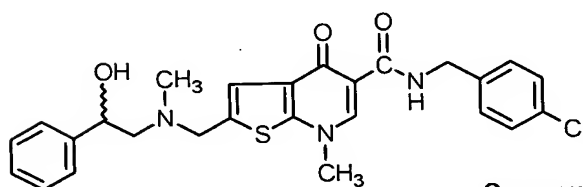
(Figure 1 continue)



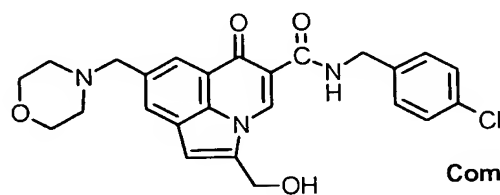
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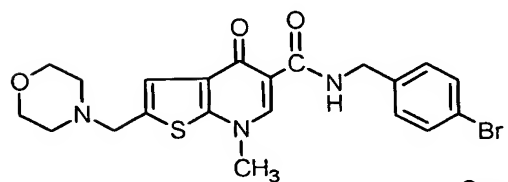
Compound No. 7



Compound No. 8

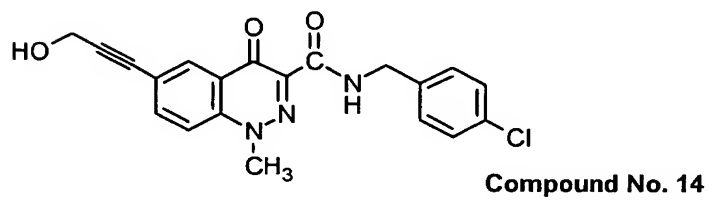
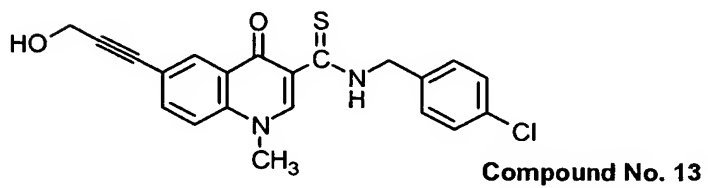
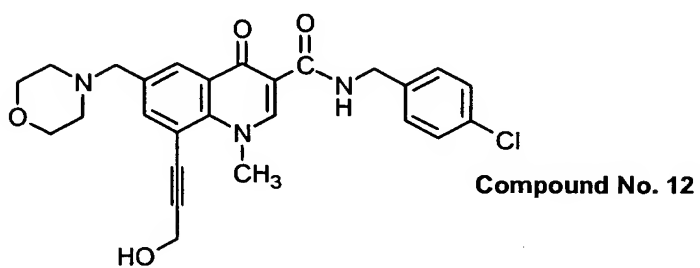
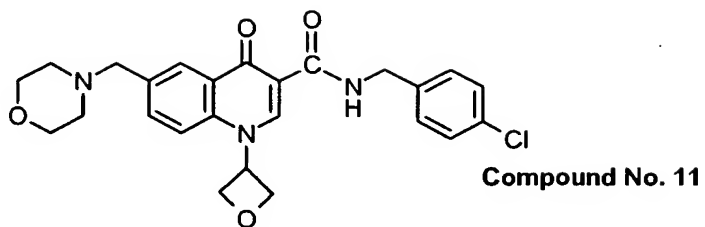


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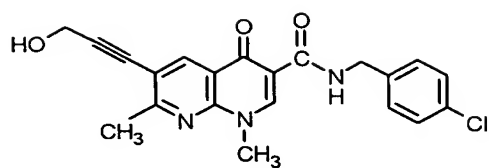


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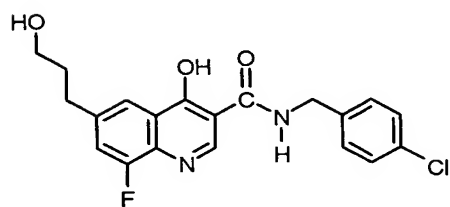
(Figure 1 continue)



(Figure 1 continue)

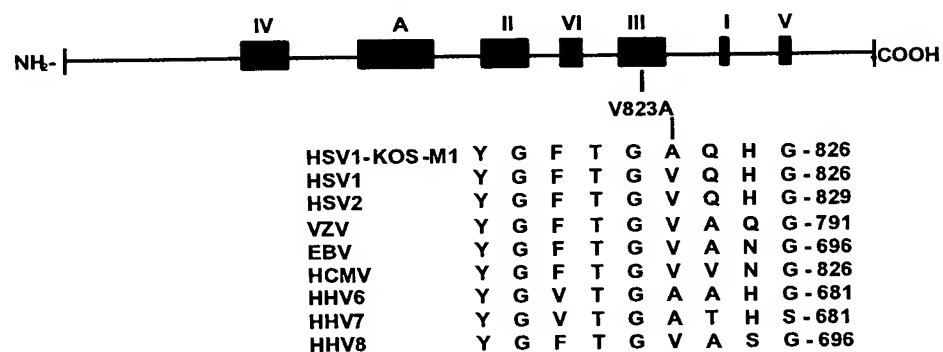


Compound No.15



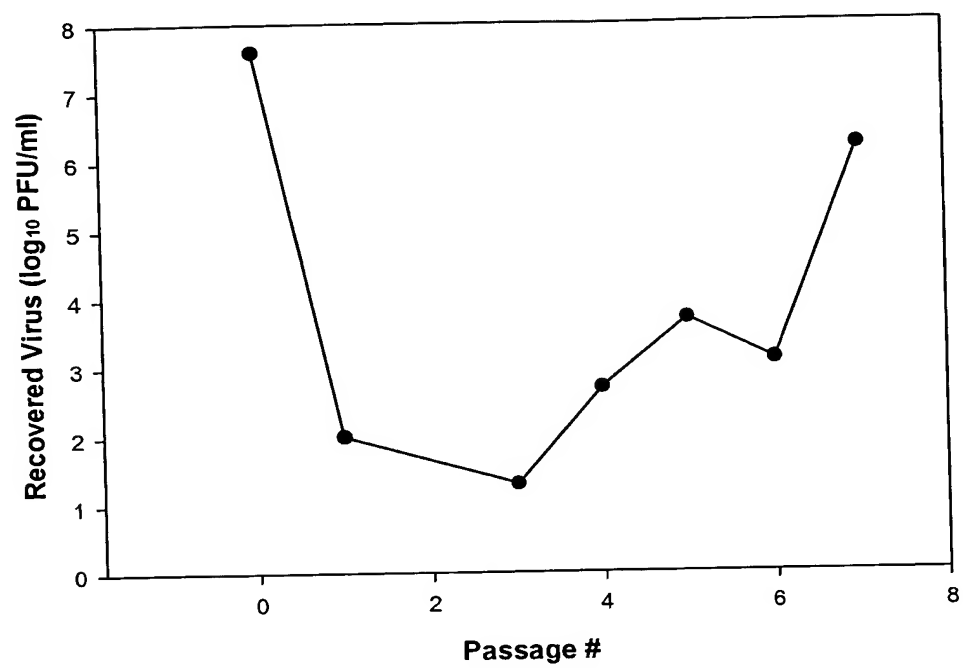
Compound 17

**Figure 2. The HSV1 (KOS Strain) DNA Polymerase Amino Acid 823 is Critical for Resistance to 4-Hydroxyquinolines and Related Compounds**



Schematic of HSV1 polymerase illustrating the conserved regions A and I-VI found in class 2 polymerases. Also shown are the amino acid sequence for the highly conserved herpesvirus domain in region III which surrounds the HSV1 amino acid 823.

**Figure 3**      **Serial Passage of HSV-1 in Presence of 20  $\mu$ M compound 17**



**Figure 4 Comparison of Wild type HSV-1 and HSV-2 DNA Polymerases Amino Acid Sequences Aligned by Amino Acid Homology\***

5	HSV2-MS	MFCAAGGPTS	PGGKSAARAA	SGFFAPHNPR	GATQTAPPPC	RRQNFYNPHL	-50
	HSV2-186	MFCAAGGPAS	PGGKSAARAA	SGFFAPHNPR	GATQTAPPPC	RRQNFYNPHL	-50
	HSV1-Kos	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GAGR.GPPPC	LRQNFYNPYL	-49
	HSV1-Patton	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GAGR.GPPPC	LRQNFYNPYL	-49
	HSV1-DJL	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GAGR.GPPPC	LRQNFYNPYL	-49
	HSV1-F	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GAGR.GPPPC	LRQNFYNPYL	-49
10	HSV2-MS	AQTGTQPKAP	GPAQRHTYYS	ECDEFRLFAP	RSLDEDAPAE	QRTGVHDGRL	-100
	HSV2-186	AQTGTQPKAP	GPAQRHTYYS	ECDEFRLFAP	RSLDEDAPAE	QRTGVHDGRL	-100
	HSV1-Kos	APVGTQQKPT	GPTQRHTYYS	ECDEFRLFAP	RVLDEDAPPE	KRAGVHDGHL	-99
	HSV1-Patton	APVGTQQKPT	GPTQRHTYYS	ECDEFRLFAP	RVLDEDAPPE	KRAGVHDGHL	-99
	HSV1-DJL	APVGTQQKPT	GPTQRHTYYS	ECDEFRLFAP	RVLDEDAPPE	KRAGVHDGHL	-99
	HSV1-F	APVGTQQKPT	GPTQRHTYYS	ECDEFRLFAP	RVLDEDAPPE	KRAGVHDGHL	-99
20	HSV2-MS	RRAPKVYCGG	DERDVLRVGP	EGFWPRRLRL	WGGADHAPKG	FDPTVTVFHV	-150
	HSV2-186	RRAPKVYCGG	DERDVLRVGP	EGFWPRRLRL	WGGADHAPKG	FDPTVTVFHV	-150
	HSV-Kos	KRAPKVYCGG	DERDVLRVGS	GGFWPRRSRL	WGGVDHAPAG	FNPTVTVFHV	-149
	HSV1-Patton	KRAPKVYCGG	DERDVLRVGS	GGFWPRRSRL	WGGVDHAPAG	FNPTVTVFHV	-149
	HSV1-DJL	KRAPKVYCGG	DERDVLRVGS	GGFWPRRSRL	WGGVDHAPAG	FNPTVTVFHV	-149
	HSV1-F	KRAPKVYCGG	DERDVLRVGS	GGFWPRRSRL	WGGVDHAPAG	FNPTVTVFHV	-149
25	HSV2-MS	YDILEHVEHA	YSMRAAQLHE	RFMDAITPAG	TVITLLGLTP	EGHRVAVHVV	-200
	HSV2-186	YDILEHVEHA	YSMRAAQLHE	RFMDAITPAG	TVITLLGLTP	EGHRVAVHVV	-200
	HSV-Kos	YDILENVEHA	YGMRAAQFHA	RFMDAITPTG	TVITLLGLTP	EGHRVAVHVV	-199
	HSV1-Patton	YDILENVEHA	YGMRAAQFHA	RFMDAITPTG	TVITLLGLTP	EGHRVAVHVV	-199
	HSV1-DJL	YDILENVEHA	YGMRAAQFHA	RFMDAITPTG	TVITLLGLTP	EGHRVAVHVV	-199
	HSV1-F	YDILENVEHA	YGMRAAQFHA	RFMDAITPTG	TVITLLGLTP	EGHRVAVHVV	-199
30	HSV2-MS	GTRQYFYMNK	AEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-250
	HSV2-186	GTRQYFYMNK	AEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-250
	HSV-Kos	GTRQYFYMNK	EEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-249
	HSV1-Patton	GTRQYFYMNK	EEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-249
	HSV1-DJL	GTRQYFYMNK	EEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-249
	HSV1-F	GTRQYFYMNK	EEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-249
35	HSV2-MS	GTRQYFYMNK	AEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-250
	HSV2-186	GTRQYFYMNK	AEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-250
	HSV-Kos	GTRQYFYMNK	EEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-249
	HSV1-Patton	GTRQYFYMNK	EEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-249
	HSV1-DJL	GTRQYFYMNK	EEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-249
	HSV1-F	GTRQYFYMNK	EEVDRHLQCR	APRDLCECLA	AALRESPGAS	FRGISADHFE	-249
40	HSV2-MS	AEVVERADVY	YYETRPTLYY	RVFVRSGRAL	AYLCDNFCEPA	IRKYEGGVDA	-300
	HSV2-186	AEVVERADVY	YYETRPTLYY	RVFVRSGRAL	AYLCDNFCEPA	IRKYEGGVDA	-300
	HSV-Kos	AEVVERTDVY	YYETRPALFY	RVYVRSGRVL	SYLCDNFCEPA	IKKYEGGVDA	-299
	HSV1-Patton	AEVVERTDVY	YYETRPALFY	RVYVRSGRVL	SYLCDNFCEPA	IKKYEGGVDA	-299
	HSV1-DJL	AEVVERTDVY	YYETRPALFY	RVYVRSGRVL	SYLCDNFCEPA	IKKYEGGVDA	-299
	HSV1-F	AEVVERTDVY	YYETRPALFY	RVYVRSGRVL	SYLCDNFCEPA	IKKYEGGVDA	-299
45	HSV2-MS	TTRFILDNPG	FVTFGWYRLK	PGRGNAPAPQ	RPPTAFGTSS	DVEFNCTADN	-350
	HSV2-186	TTRFILDNPG	FVTFGWYRLK	PGRGNAPAPQ	RPPTAFGTSS	DVEFNCTADN	-350
	HSV-Kos	TTRFILDNPG	FVTFGWYRLK	PGRNNTLAQP	RAPMAFGTSS	DVEFNCTADN	-349
	HSV1-Patton	TTRFILDNPG	FVTFGWYRLK	PGRNNTLAQP	RAPMAFGTSS	DVEFNCTADN	-349
	HSV1-DJL	TTRFILDNPG	FVTFGWYRLK	PGRNNTLAQP	RAPMAFGTSS	DVEFNCTADN	-349
	HSV1-F	TTRFILDNPG	FVTFGWYRLK	PGRNNTLAQP	RAPMAFGTSS	DVEFNCTADN	-349
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	HSV1-F	TTRFILDNPG	FVTFGWYRLK	PGRNNTLAQP	RAPMAFGTSS	DVEFNCTADN	-349
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	HSV1-Patton	LAIEGGMSDL	PAYKLMCFDI	ECKAGGEDEL	AFPVAGHPED	LVIQISCLLY	-399
	HSV1-DJL	LAIEGGMSDL	PAYKLMCFDI	ECKAGGEDEL	AFPVAGHPED	LVIQISCLLY	-399
	HSV1-F	LAIEGGMSDL	PAYKLMCFDI	ECKAGGEDEL	AFPVAGHPED	LVIQISCLLY	-399
60	HSV2-MS	DLSTTALEHI	LLFSLGSCDL	PESHLSDLAS	RGLPAPVVLE	FDSEFEMLLA	-450
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	HSV-Kos	DLSTTALEHV	LLFSLGSCDL	PESHLNELAA	RGLPTPVVLE	FDSEFEMLLA	-449
	HSV1-Patton	DLSTTALEHV	LLFSLGSCDL	PESHLNELAA	RGLPTPVVLE	FDSEFEMLLA	-449
	HSV1-DJL	DLSTTALEHV	LLFSLGSCDL	PESHLNELAA	RGLPTPVVLE	FDSEFEMLLA	-449
	HSV1-F	DLSTTALEHV	LLFSLGSCDL	PESHLNELAA	RGLPTPVVLE	FDSEFEMLLA	-449

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	HSV2-186	FMTFVKQYGP	EFVTGYNIIN	FDWPFVLTCL	TEIYKVPLDG	YGRMNNGRVF	-500
	HSV-Kos	FMTLVKQYGP	EFVTGYNIIN	FDWPFLLAKL	TDIYKVPLDG	YGRMNNGRVF	-499
	HSV1-Patton	FMTLVKQYGP	EFVTGYNIIN	FDWPFLLAKL	TDIYKVPLDG	YGRMNNGRVF	-499
	HSV1-DJL	FMTLVKQYGP	EFVTGYNIIN	FDWPFLLAKL	TDIYKVPLDG	YGRMNNGRVF	-499
	HSV1-F	FMTLVKQYGP	EFVTGYNIIN	FDWPFLLAKL	TDIYKVPLDG	YGRMNNGRVF	-499
10	HSV2-MS	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKVKLSSYK	LNAVAEAVLK	-550
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	HSV-Kos	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKIKLSSYK	LNAVAEAVLK	-549
	HSV1-Patton	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKIKLSSYK	LNAVAEAVLK	-549
	HSV1-DJL	RVWDIGQSHF	QKRSKIKVNG	MVNIDMYGII	TDKIKLSSYK	LNAVAEAVLK	-549
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	HSV2-186	DKKKDLSYRD	IPAYYASGPA	QRGVIGEYCV	QDSLLVGQLF	FKFLPHLELS	-600
	HSV-Kos	DKKKDLSYRD	IPAYYAAGPA	QRGVIGEYCI	QDSLLVGQLF	FKFLPHLELS	-599
	HSV1-Patton	DKKKDLSYRD	IPAYYAAGPA	QRGVIGEYCI	QDSLLVGQLF	FKFLPHLELS	-599
	HSV1-DJL	DKKKDLSYRD	IPAYYAAGPA	QRGVIGEYCI	QDSLLVGQLF	FKFLPHLELS	-599
	HSV1-F	DKKKDLSYRD	IPAYYAAGPA	QRGVIGEYCI	QDSLLVGQLF	FKFLPHLELS	-599
25	HSV2-MS	AVARLAGINI	TRTIYDGQOI	RVFTCLLRLL	GQKGFILPDT	QGRFRGLDKE	-650
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	HSV-Kos	AVARLAGINI	TRTIYDGQOI	RVFTCLLRLL	DQKGFILPDT	QGRFRGAGGE	-649
	HSV1-Patton	AVARLAGINI	TRTIYDGQOI	RVFTCLLRLL	DQKGFILPDT	QGRFRGAGGE	-649
	HSV1-DJL	AVARLAGINI	TRTIYDGQOI	RVFTCLLRLL	DQKGFILPDT	QGRFRGAGGE	-649
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	HSV-Kos	APKRPAARE	DEERP.....	EEGEDEDER	EEGGGEREPE	GARETAGRHV	-694
	HSV1-Patton	APKRPAARE	DEERP.....	EEGEDEDER	EEGGGEREPE	GARETAGRHV	-694
	HSV1-DJL	APKRPAARE	DEERP.....	EEGEDENER	EEGGGEREPE	GARETAGRHV	-694
	HSV1-F	APKRPAARE	DEERP.....	EEGEDEDER	EEGGGEREPE	GARETAGRHV	-694
40	HSV2-MS	GYQGARVLDP	TSGFHVDPVV	VDFASLYPS	IIQAHNLCFS	TLSLRPEAVA	-747
	HSV2-186	GYQGARVLDP	TSGFHVDPVV	VDFASLYPS	IIQAHNLCFS	TLSLRPEAVA	-749
	HSV-Kos	GYQGARVLDP	TSGFHVNPVV	VDFASLYPS	IIQAHNLCFS	TLSLRADAVA	-744
	HSV1-Patton	GYQGARVLDP	ISGFHVNPVV	VDFASLYPS	IIQAHNLCFS	TLSLRADAVA	-744
	HSV1-DJL	GYQGARVLDP	TSGFHVNPVV	VDFASLYPS	IIQAHNLCFS	TLSLRADAVA	-744
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45	HSV2-MS	HLEARDYLE	IEVGRRRLFF	VKAHVRESLL	SILLRDWLAM	RKQIRSRIPQ	-797
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	HSV-Kos	HLEAGDYLE	IEVGRRRLFF	VKAHVRESLL	SILLRDWLAM	RKQIRSRIPQ	-794
	HSV1-Patton	HLEAGDYLE	IEVGRRRLFF	VKAHVRESLL	SILLRDWLAM	RKQIRSRIPQ	-794
	HSV1-DJL	HLEAGDYLE	IEVGRRRLFF	VKAHVRESLL	SILLRDWLAM	RKQIRSRIPQ	-794
	HSV1-F	HLEAGDYLE	IEVGRRRLFF	VKAHVRESLL	SILLRDWLAM	RKQIRSRIPQ	-794
50	HSV2-MS	STPEEAVLLD	KQQAIAKVVC	NSVYGFTGVQ	HGLLPCLHVA	ATVTTIGREM	-847
	HSV2-186	SPPEEAVLLD	KQQAIAKVVC	NSVYGFTGVQ	HGLLPCLHVA	ATVTTIGREM	-849
	HSV-Kos	SSPEEAVLLD	KQQAIAKVVC	NSVYGFTGVQ	HGLLPCLHVA	ATVTTIGREM	-844
	HSV1-Patton	SSPEEAVLLD	KQQAIAKVVC	NSVYGFTGVQ	HGLLPCLHVA	ATVTTIGREM	-844
	HSV1-DJL	SSPEEAVLLD	KQQAIAKVVC	NSVYGFTGVQ	HGLLPCLHVA	ATVTTIGREM	-844
	HSV1-F	SSPEEAVLLD	KQQAIAKVVC	NSVYGFTGVQ	HGLLPCLHVA	ATVTTIGREM	-844
60	HSV2-MS	LLATRAYVHA	RWAEFDQLLA	DFPEAAGMRA	PGPYSMRIY	GDTDSIFVLC	-897
	HSV2-186	LLATRAYVHA	RWAEFDQLLA	DFPEAAGMRA	PGPYSMRIY	GDTDSIFVLC	-899
	HSV-Kos	LLATREYVHA	RWAAFEQLLA	DFPEADMRA	PGPYSMRIY	GDTDSIFVLC	-894
	HSV1-Patton	LLATREYVHA	RWAAFEQLLA	DFPEADMRA	PGPYSMRIY	GDTDSIFVLC	-894
	HSV1-DJL	LLATREYVHA	RWAAFEQLLA	DFPEADMRA	PGPYSMRIY	GDTDSIFVLC	-894
	HSV1-F	LLATREYVHA	RWAAFEQLLA	DFPEADMRA	PGPYSMRIY	GDTDSIFVLC	-894
65	HSV2-MS	RGLTAAGLVA	MGDKMASHIS	RALFLPPIKL	ECEKTFTKLL	LIAKKYYIGV	-947



	HSV2-186	RGLTAAGLVA	MGDKMASHIS	RALFLPPIKL	ECEKTFTKLL	LIAKKKYIGV	-949
	HSV-Kos	RGLTAAGLTA	MGDKMASHIS	RALFLPPIKL	ECEKTFTKLL	LIAKKKYIGV	-944
	HSV1-Patton	RGLTAAGLTA	MGDKMASHIS	RALFLPPIKL	ECEKTFTKLL	LIAKKKYIGV	-944
	HSV1-DJL	RGLTAAGLTA	VGDKMASHIS	RALFLPPIKL	ECEKTFTKLL	LIAKKKYIGV	-944
5	HSV1-F	RGLTAAGLTA	VGDKMASHIS	RALFLSPIKL	ECEKTFTKLL	LIAKKKYIGV	-944
	HSV2-MS	ICGGKMLIKG	VDLVRKNNCA	FINRTSRALV	DLLFYDDTVS	GAAAAALAERP	-997
	HSV2-186	ICGGKMLIKG	VDLVRKNNCA	FINRTSRALV	DLLFYDDTVS	GAAAAALAERP	-999
	HSV-Kos	IYGGKMLIKG	VDLVRKNNCA	FINRTSRALV	DLLFYDDTVS	GAAAAALAERP	-994
10	HSV1-Patton	IYGGKMLIKG	VDLVRKNNCA	FINRTSRALV	DLLFYDDTVS	GAAAAALAERP	-994
	HSV1-DJL	IYGGKMLIKG	VDLVRKNNCA	FINRTSRALV	DLLFYDDTVS	GAAAAALAERP	-994
	HSV1-F	IYGGKMLIKG	VDLVRKNNCA	FINRTSRALV	DLLFYDDTVS	GAAAAALAERP	-994
	HSV2-MS	AEEWLARPLP	EGLQAFGAVL	VDAHRRITDP	ERDIQDFVLT	AELSRHPRAY	-1047
15	HSV2-186	AEEWLARPLP	EGLQAFGAVL	VDAHRRITDP	ERDIQDFVLT	AELSRHPRAY	-1049
	HSV-Kos	AEEWLARPLP	EGLQAFGAVL	VDAHRRITDP	ERDIQDFVLT	AELSRHPRAY	-1044
	HSV1-Patton	AEEWLARPLP	EGLQAFGAVL	VDAHRRITDP	ERDIQDFVLT	AELSRHPRAY	-1044
	HSV1-DJL	AEEWLARPLP	EGLQAFGAVL	VDAHRRITDP	ERDIQDFVLT	AELSRHPRAY	-1044
	HSV1-F	AEEWLARPLP	EGLQAFGAVL	VDAHRRITDP	ERDIQDFVLT	AELSRHPRAY	-1044
20	HSV2-MS	TNKRLAHLTV	YYKLMARRAQ	VPSIKDRIPY	VIVAQTREVE	ETVARLAALR	-1097
	HSV2-186	TNKRLAHLTV	YYKLMARRAQ	VPSIKDRIPY	VIVAQTREVE	ETVARLAALR	-1099
	HSV-Kos	TNKRLAHLTV	YYKLMARRAQ	VPSIKDRIPY	VIVAQTREVE	ETVARLAALR	-1094
	HSV1-Patton	TNKRLAHLTV	YYKLMARRAQ	VPSIKDRIPY	VIVAQTREVE	ETVARLAALR	-1094
25	HSV1-DJL	TNKRLAHLTV	YYKLMARRAQ	VPSIKDRIPY	VIVAQTREVE	ETVARLAALR	-1094
	HSV1-F	TNKRLAHLTV	YYKLMARRAQ	VPSIKDRIPY	VIVAQTREVE	ETVARLAALR	-1094
	HSV2-MS	ELDAAAPGDE	PAPPAALPSP	AKRPRETPSH	ADPPGGASKP	RKLLVSELAE	-1147
	HSV2-186	ELDAAAPGDE	PAPPAALPSP	AKRPRETPSH	ADPPGGASKP	RKLLVSELAE	-1149
30	HSV-Kos	ELDAAAPGDE	PAPPAALPSP	AKRPRETPSH	ADPPGGASKP	RKLLVSELAE	-1144
	HSV1-Patton	ELDAAAPGDE	PAPPAALPSP	AKRPRETPSP	ADPPGGASKP	RKLLVSELAE	-1144
	HSV1-DJL	ELDAAAPGDE	PAPPAALPSP	AKRPRETPSP	ADPPGGASKP	RKLLVSELAE	-1144
	HSV1-F	ELDAAAPGDE	PAPPAALPSP	AKRPRETPLH	ADPPGGASKP	RKLLVSELAE	-1144
35	HSV2-MS	DPGYAIARGV	PLNTDYYFSH	LLGAACVTFK	ALFGNNAKIT	ESLLKRFIPE	-1197
	HSV2-186	DPGYAIARGV	PLNTDYYFSH	LLGAACVTFK	ALFGNNAKIT	ESLLKRFIPE	-1199
	HSV-Kos	DPAYAIAHGV	ALNTDYYFSH	LLGAACVTFK	ALFGNNAKIT	ESLLKRFIPE	-1194
	HSV1-Patton	DPAYAIAHGV	ALNTDYYFSH	LLGAACVTFK	ALFGNNAKIT	ESLLKRFIPE	-1194
	HSV1-DJL	DPAYAIAHGV	ALNTDYYFSH	LLGAACVTFK	ALFGNNAKIT	ESLLKRFIPE	-1194
40	HSV1-F	DPAYAIAHGV	ALNTDYYFSH	LLGAACVTFK	ALFGNNAKIT	ESLLKRFIPE	-1194
	HSV2-MS	TWHPPDDVAA	RLRAAGFGPA	GAGATAEETR	RMLHRAFDTL	A* -1238	
	HSV2-186	TWHPPDDVAA	RLRAAGFGPA	GAGATAEETR	RMLHRAFDTL	A* -1240	
	HSV-Kos	VWHPPDDVAA	RLRAAGFGAV	GAGATAEETR	RMLHRAFDTL	A* -1235	
45	HSV1-Patton	VWHPPDDVTA	RLRAAGFGAV	GAGATAEETR	RMLHRAFDTL	A* -1235	
	HSV1-DJL	VWHPPDDVAA	RLRTAGFGAV	GAGATAEETR	RMLHRAFDTL	A* -1235	
	HSV1-F	VWHPPDDVAA	RLRAAGFGAV	GAGATAEETR	RMLHRAFDTL	A* -1235	

\*Amino acid alignment demonstrates difference in amino acid's sequences.

50 \*The gaps "....." indicate missing amino acids relative to other stanins.

\*Wild HSV2-MS is listed as SEQ. ID NO 14.

\*Wild HSV2-186 is listed as SEQ. ID NO 15.

\*Wild HSV-Kos is listed as SEQ. ID NO 16.

\*Wild HSV1-Patton is listed as SEQ. ID NO 17.

55 \*Wild HSV1-DJL is listed as SEQ. ID NO 18.

\*Wild HSV1-F is listed as SEQ. ID NO 19.

**Figure 5 DNA and amino acid sequence list****SEQ. ID. NO. 1** DNA sequence of DNA polymerase gene for HSV2-MS-M1

5 1 ATGTTTTGTG CCGCGGGCGG CCCGACTTCC CCCGGGGGGA AGTCGGCGGC  
 51 TCGGGCGGCG TCTGGGTTTT TTGCCCCCA CAACCCCGG GGAGCCACCC  
 10 101 AGACGGCACC GCCGCCTTGC CGCCGGCAGA ACTTCTACAA CCCCACCTC  
 151 GCTCAGACCG GAACGCAGCC AAAGGCCCCC GGGCCGGCTC AGCGCCATAC  
 201 GTACTACAGC GAGTGCGACG AATTTCGATT TATCGCCCCG CGTTCGCTGG  
 15 251 ACGAGGACGC CCCC GCGGAG CAGCGCACC GGGTCCACGA CGGCCGCCTC  
 301 CGGCGCGCCC CTAAGGTGTA CTGCGGGGGG GACGAGCGCG ACGTCCTCCG  
 20 351 CGTGGGCCCC GAGGGCTTCT GGCCGCGTCG CTTGCGCCTG TGGGGCGGTG  
 401 CGGACCATGC CCCCAAGGGG TTCGACCCA CCGTCACCGT CTTCCACGTG  
 451 TACGACATCC TGGAGCACGT GGAACACGCG TACAGCATGC GCGCCGCCCA  
 25 501 GCTCCACGAG CGATTTATGG ACGCCATCAC GCCCGCCGGG ACCGTCATCA  
 551 CGCTTCTGGG TCTGACCCCC GAAGGCCATC GCGTCGCCGT TCACGTCTAC  
 30 601 GGCACGCGGC AGTACTTTTA CATGAACAAG GCGGAGGTGG ATCGGCACCT  
 651 GCAGTGCCGT GCCCGCGCG ATCTCTGCGA GCGCCTGGCG GCGGCCCTGC  
 701 GCGAGTCGCC GGGGGCGTCG TTCCGCGGCA TCTCCGCGGA CCACTTCGAG  
 35 751 GCGGAGGTGG TGGAGCGCGC CGACGTGTAC TATTACGAAA CGCGCCCGAC  
 801 CCTGTACTAC CGCGTCTTCG TGC GAAGCGG GCGCGCGCTG GCCTACCTGT  
 40 851 GCGACA ACTT TTGCCCCGCG ATCAGGAAGT ACGAGGGGGG CGTCGACGCC  
 901 ACCACCCGGT TTATCCTGGA CAACCCGGGG TTTGTACCT TCGGCTGGTA  
 951 CCGCCTCAAG CCCGGCCGCG GGAACGCGCC GGCCCAACCG CGCCCCCGA  
 45 1001 CGGCGTTCGG AACCTCGAGC GACGTCGAGT TTA ACTGCAC GCGGACAAC  
 1051 CTGGCCGTCG AGGGGGCCAT GTGTGACCTG CCGGCCTACA AGCTCATGTG  
 50 1101 CTTCGATATC GAATGCAAGG CCGGGGGGGA GGACGAGCTG GCCTTTCCGG  
 1151 TCGCGGAACG CCCGGAAGAC CTCGTCATCC AGATCTCCTG TCTGCTCTAC  
 1201 GACCTGTCCA CCACCGCCCT CGAGCACATC CTCCTGTTTT CGCTCGGATC  
 55 1251 CTGCGACCTC CCCGAGTCCC ACCTCAGCGA TCTCGCCTCC AGGGGCCTGC

1301 CGGCCCCCGT CGTCCTGGAG TTTGACAGCG AATTCGAGAT GCTGCTGGCC  
 1351 TTCATGACCT TCGTCAAGCA GTACGGCCCC GAGTTCGTGA CCGGGTACAA  
 5 1401 CATCATCAAC TTCGACTGGC CCTTCGTCCT GACCAAGCTG ACGGAGATCT  
 1451 ACAAGGTCCC GCTCGACGGG TACGGGCGCA TGAACGGCCG GGGTGTGTTC  
 1501 CGCGTGTGGG ACATCGGCCA GAGCCACTTT CAGAAGCGCA GCAAGATCAA  
 10 1551 GGTGAACGGG ATGGTGAACA TCGACATGTA CGGCATCATC ACCGACAAGG  
 1601 TCAAACCTCTC CAGCTACAAG CTGAACGCCG TCGCCGAGGC CGTCTTGAAG  
 1651 GACAAGAAGA AGGATCTGAG CTACCGCGAC ATCCCCGCCT ACTACGCCTC  
 1701 CGGGCCCGCG CAGCGCGGGG TGATCGGCGA GTATTGTGTG CAGGACTCGC  
 1751 TGCTGGTCGG GCAGCTGTTC TTCAAGTTTC TGCCGCACCT GGAGCTTTCC  
 20 1801 GCCGTCGCGC GCCTGGCGGG CATCAACATC ACCCGCACCA TCTACGACGG  
 1851 CCAGCAGATC CGCGTCTTCA CGTGCCTCCT GCGCCTTGCG GGCCAGAAGG  
 25 1901 GCTTCATCCT GCCGGACACC CAGGGGCGGT TTCGGGGCCT CGACAAGGAG  
 1951 GCGCCCAAGC GCCCGGCCGT GCCTCGGGGG GAAGGGGAGC GGCCGGGGGA  
 2001 CGGGAACGGG GACGAGGATA AGGACGACGA CGAGGACGAG GACGGGGACG  
 30 2051 AGCGCGAGGA GGTCGCGCGC GAGACCGGGG GCCGGCACGT TGGGTACCAG  
 2101 GGGGCCCCGG TCCTCGACCC CACCTCCGGG TTTCACGTG ACCTCGTGGT  
 35 2151 GGTGTTTGAC TTTGCCAGCC TGTACCCAG CATCATCCAG GCCACAACC  
 2201 TGTGCTTCAG TACGCTCTCC CTGCGGCCCG AGGCCGTGCG GCACCTGGAG  
 2251 GCGGACCGGG ACTACCTGGA GATCGAGGTG GGGGGCCGAC GGCTGTTCTT  
 40 2301 CGTGAAGGCC CACGTACGCG AGAGCCTGCT GAGCATCCTG CTGCGCGACT  
 2351 GGCTGGCCAT GCGAAAGCAG ATCCGCTGCG GGATCCCCCA GAGCACCCCC  
 45 2401 GAGGAGGCCG TCCTCCTCGA CAAGCAACAG GCCGCCATCA AGGTGGTGTG  
 2451 CAACTCGGTG TACGGGTTCA CCGGGGCGCA GCACGGTCTT CTGCCCTGCC  
 2501 TGCACGTGGC CGCCACCGTG ACGACCATCG GCCGCGAGAT GCTCCTCGCG  
 50 2551 ACGCGCGCGT ACGTGACGC GCGCTGGGCG GAGTTCGATC AGCTGCTGGC  
 2601 CGACTTTCCG GAGGCGGCCG GCATGCGCGC CCCCAGTCCG TACTCCATGC  
 55 2651 GCATCATCTA CGGGGACACG GACTCCATTT TCGTTTTGTG CCGCGGCCTC  
 2701 ACGGCCGCGG GCCTGGTGGC CATGGGCGAC AAGATGGCGA GCCACATCTC  
 2751 GCGCGCGCTG TTCCTCCCC CGATCAAGCT CGAGTGCGAA AAAACGTTCA

2801 CCAAGCTGCT GCTCATCGCC AAGAAAAAGT ACATCGGCGT CATCTGCGGG  
2851 GGCAAGATGC TCATCAAGGG CGTGGATCTG GTGCGCAAAA ACAACTGCGC  
5 2901 GTTTATCAAC CGCACCTCCA GGGCCCTGGT CGACCTGCTG TTTACGACG  
2951 ATACCGTATC CGGAGCGGCC GCCGCGTTAG CCGAGCGCCC CGCAGAGGAG  
10 3001 TGGCTGGCGC GACCCCTGCC CGAGGGACTG CAGGCGTTCG GGGCCGTCTT  
3051 CGTAGACGCC CATCGGCGCA TCACCGACCC GGAGAGGGAC ATCCAGGACT  
3101 TTGTCCTCAC CGCCGAACTG AGCAGACACC CGCGCGCGTA CACCAACAAG  
15 3151 CGCCTGGCCC ACCTGACGGT GTATTACAAG CTCATGGCCC GCCGCGCGCA  
3201 GGTCCCGTCC ATCAAGGACC GGATCCCGTA CGTGATCGTG GCCCAGACCC  
20 3251 GCGAGGTAGA GGAGACGGTC GCGCGGCTGG CCGCCCTCCG CGAGCTAGAC  
3301 GCCGCCGCCC CAGGGGACGA GCCCGCCCCC CCAGCGGCCC TGCCCTCCCC  
3351 GGCCAAGCGC CCCCAGGAGA CGCCGTCGCA TGCCGACCCC CCGGGAGGCG  
25 3401 CGTCCAAGCC CCGCAAGCTG CTGGTGTCCG AGCTGGCGGA GGATCCCGGG  
3451 TACGCCATCG CCCGGGGCGT TCCGCTCAAC ACGGACTATT ACTTCTCGCA  
30 3501 CCTGCTGGGG GCGGCCTGCG TGACGTTCAA GGCCCTGTTT GGAAATAACG  
3551 CCAAGATCAC CGAGAGTCTG TTAAAGAGGT TTATTCCCGA GACGTGGCAC  
3601 CCCCCGGACG ACGTGGCCGC GCGGCTCAGG GCCGCGGGGT TCGGGCCGGC  
35 3651 GGGGGCCGGC GCTACGGCGG AGGAAACTCG TCGAATGTTG CATAGAGCCT  
3701 TTGATACTCT AGCATGA  
40

**SEQ. ID. NO. 2**      Amino acid sequence of DNA polymerase for HSV2-MS-M1

1 MFCAAGGPTS PGGKSAARAA SGFFAPHNPR GATQTAPPPC RRQNFYNPHL  
 5 51 AQTGTQPKAP GPAQRHTYYS ECDEFRIAP RSLDEDAPAE QRTGVHDGRL  
 101 RRAPKVYCGG DERDVLRVGP EGFWRRLRL WGGADHAPKG FDPTVTVFHV  
 151 YDILEHVEHA YSMRAAQLHE RFMDAITPAG TVITLLGLTP EGHRAVAVHY  
 10 201 GTRQYFYMNK AEVDRHLQCR APRDLCERLA AALRESPGAS FRGISADHFE  
 251 AEVVERADVY YYETRPTLYY RVFVRSRAL AYLCDNFCPA IRKYEGGVDA  
 15 301 TTRFILDNPG FVTFGWYRLK PGRGNAPAP RPPTAFGTSS DVEFNCTADN  
 351 LAVEGAMCDL PAYKLMCFDI ECKAGGEDEL AFPVAERPED LVIQISCLLY  
 401 DLSTTALEHI LLFSLGSCDL PESHLSDLAS RGLPAPVVLE FDSEFEMLLA  
 20 451 FMTFVKQYGP EFVTGYNIN FDWPFVLTCL TEIYKVPLDG YGRMNNGRGVF  
 501 RVWDIGQSHF QKRSKIKNVNG MVNIDMYGII TDKVKLSSYK LNAVAEAVLK  
 25 551 DKKKDLSDYRD IPAYYASGPA QRGVIGEYCV QDSLLVGQLF FKFLPHLELS  
 601 AVARLAGINI TRTIYDGQOI RVFTCLLRLA GQKGFILPDT QGRFRGLDKE  
 651 APKRAVPRG EGERPGDGNG DEDKDDDEDE DGDEREVAR ETGGRHVGYQ  
 30 701 GARVLDPTSG FHVDPVVVFD FASLYPSIIQ AHNLCFSTLS LRPEAVAHLE  
 751 ADRDYLEIEV GGRRLFFVKA HVRESLLSIL LRDWLAMRKQ IRSRIPQSTP  
 35 801 EEAVLLDKQQ AAIKVCNSV YGFTGAQHGL LPCLHVAATV TTIGREMLLA  
 851 TRAYVHARWA EFDQLLADFP EAAGMRAPGP YSMRIYGDY DSIFVLCRGL  
 901 TAAGLVAMGD KMASHISRAL FLPIKLECE KTFTKLLLIA KKKYIGVICG  
 40 951 GKMLIKGVDL VRKNNCAFIN RTSRALVDLL FYDDTVSGAA AALAERPAEE  
 1001 WLARPLPEGL QAFGAVLVDA HRRITDPERD IQDFVLTAEL SRHPRAYTNK  
 45 1051 RLAHLTVYYK LMARRAQVPS IKDRIPYVIV AQTREVEETV ARLAALRELD  
 1101 AAPGDEPAP PAALPSPAKR PRETPSHADP PGGASKPRKL LVSELAEDPG  
 1151 YAIARGVPLN TDYYFSHLLG AACVTFKALF GNNAKITESL LKRFPETWH  
 50 1201 PPDDVAARLR AAGFGPAGAG ATAEETRRML HRAFDTLA\*

**SEQ.ID.NO. 3**      DNA sequence of DNA polymerase gene for HSV2-186-M1

1 ATGTTTTGTG CCGCGGGCGG CCCGGCTTCC CCCGGGGGGA AGTCGGCGGC  
 5 51 TCGGGCGGCG TCTGGGTTTT TTGCCCCCA CAACCCCGG GGAGCCACCC  
 101 AGACGGCACC GCCGCCTTGC CGCCGGCAGA ACTTCTACAA CCCCCACCTC  
 151 GCTCAGACCG GAACGCAGCC AAAGGCCCCC GGGCCGGCTC AGCGCCATAC  
 10 201 GTACTACAGC GAGTGCGACG AATTTGATT TATCGCCCCG CGTTCGCTGG  
 251 ACGAGGACGC CCCCGCGGAG CAGCGCACCG GGGTCCACGA CGGCCGCCTC  
 15 301 CGGCGCGCCC CTAAGGTGTA CTGCGGGGGG GACGAGCGCG ACGTCTCCG  
 351 CGTGGGCCCC GAGGGCTTCT GGCCGCGTCG CTTGCGCCTG TGGGGCGGTG  
 401 CGGACCATGC CCCCGAGGGG TTCGACCCA CCGTCACCGT CTTCCACGTG  
 20 451 TACGACATCC TGGAGCACGT GGAACACGCG TACAGCATGC GCGCCGCCCA  
 501 GCTCCACGAG CGATTTATGG ACGCCATCAC GCCCGCCGGG ACCGTCATCA  
 25 551 CGCTTCTGGG TCTGACCCCC GAAGGCCATC GCGTCGCCGT TCACGTCTAC  
 601 GGCACGCGGC AGTACTTTTA CATGAACAAG GCGGAGGTGG ATCGGCACCT  
 651 GCAGTGCCGT GCCCCGCGCG ATCTCTGCGA GCGCCTGGCG GCGGCCCTGC  
 30 701 GCGAGTCGCC GGGGGCGTCG TTCCGCGGCA TCTCCGCGGA CCACTTCGAG  
 751 GCGGAGGTGG TGGAGCGCGC CGACGTGTAC TATTACGAAA CGCGCCCGAC  
 35 801 CCTGTACTAC CGCGTCTTCG TGCGAAGCGG GCGCGCGCTG GCCTACCTGT  
 851 GCGACAATT TTGCCCCGCG ATCAGGAAGT ACGAGGGGGG CGTCGACGCC  
 901 ACCACCCGGT TTATCCTGGA CAACCCGGGG TTTGTACCT TCGGCTGGTA  
 40 951 CCGCCTCAAG CCCGGCCGCG GGAACGCGCC GGCCCAACCG CGCCCCCGA  
 1001 CGGCGTTCGG AACCTCGAGC GACGTCGAGT TTAAGTGCAC GGCGGACAAC  
 45 1051 CTGGCCGTCG AGGGGGCCAT GTGTGACCTG CCGGCCTACA AGCTCATGTG  
 1101 CTTGATATC GAATGCAAGG CCGGGGGGGA GGACGAGCTG GCCTTTCCGG  
 1151 TCGCGGAACG CCCGGAAGAC CTCGTCATCC AGATCTCCTG TCTGCTCTAC  
 50 1201 GACCTGTCCA CCACCGCCCT CGAGCACATC CTCCTGTTTT CGCTCGGATC  
 1251 CTGCGACCTC CCCGAGTCCC ACCTCAGCGA TCTCGCCTCC AGGGGCCTGC  
 55 1301 CGGCCCCCGT CGTCTGGAG TTTGACAGCG AATTCGAGAT GCTGCTGGCC  
 1351 TTCATGACCT TCGTCAAGCA GTACGGCCCC GAGTTCGTGA CCGGGTACAA  
 1401 CATCATCAAC TTCGACTGGC CCTTCGTCTT GACCAAGCTG ACGGAGATCT

1451 ACAAGGTCCC GCTCGACGGG TACGGGCGCA TGAACGGCCG GGGTGTGTTC  
 1501 CGCGTGTGGG ACATCGGCCA GAGCCACTTT CAGAAGCGCA GCAAGATCAA  
 5 1551 GGTGAACGGG ATGGTGAACA TCGACATGTA CGGCATCATC ACCGACAAGG  
 1601 TCAAACCTCTC CAGCTACAAG CTGAACGCCG TCGCCGAGGC CGTCTTGAAG  
 10 1651 GACAAGAAGA AGGATCTGAG CTACCGCGAC ATCCCCGCCT ACTACGCCTC  
 1701 CGGGCCCCGCG CAGCGCGGGG TGATCGGCGA GTATTGTGTG CAGGACTCGC  
 1751 TGCTGGTCGG GCAGCTGTTC TTCAAGTTTC TGCCGCACCT GGAGCTTTCC  
 15 1801 GCCGTCGCGC GCCTGGCGGG CATCAACATC ACCCGCACCA TCTACGACGG  
 1851 CCAGCAGATC CGCGTCTTCA CGTGCCTCCT GCGCCTTGCG GGCCAGAAGG  
 20 1901 GCTTCATCCT GCCGGACACC CAGGGGCGGT TTCGGGGCCT CGACAAGGAG  
 1951 GCGCCCAAGC GCCCGGCCGT GCCTCGGGGG GAAGGGGAGC GGCCGGGGGA  
 2001 CGGGAACGGG GACGAGGATA AGGACGACGA CGAGGACGGG GACGAGGACG  
 25 2051 GGGACGAGCG CGAGGAGGTC GCGCGCGAGA CCGGGGGCCG GCACGTTGGG  
 2101 TACCAGGGGG CCCGGGTCCT CGACCCACC TCCGGGTTTC ACGTCGACCC  
 30 2151 CGTGGTGGTG TTTGACTTTG CCAGCCTGTA CCCCAGCATC ATCCAGGCCC  
 2201 ACAACCTGTG CTTCAGTACG CTCTCCCTGC GGCCCGAGGC CGTCGCGCAC  
 2251 CTGGAGGCGG ACCGGGACTA CCTGGAGATC GAGGTGGGGG GCCGACGGCT  
 35 2301 GTTCTTCGTG AAGGCCACG TACGCGAGAG CCTGCTGAGC ATCCTGCTGC  
 2351 GCGACTGGCT GGCCATGCGA AAGCAGATCC GCTCGCGGAT CCCCCAGAGC  
 40 2401 CCCCCGAGG AGGCCGTCCT CCTCGACAAG CAACAGGCCG CCATCAAGGT  
 2451 GGTGTGCAAC TCGGTGTACG GGTTCACCGG GCGCGAGCAC GGTCTTCTGC  
 2501 CCTGCCTGCA CGTGGCCGCC ACCGTGACGA CCATCGGCCG CGAGATGCTC  
 45 2551 CTCGCGACGC GCGCGTACGT GCACGCGCGC TGGGCGGAGT TCGATCAGCT  
 2601 GCTGGCCGAC TTCCGGAGG CGGCCGGCAT GCGCGCCCCC GGTCCGTACT  
 50 2651 CCATGCGCAT CATCTACGGG GACACGGA CTATTTTCGT TTTGTGCCGC  
 2701 GGCCTCACGG CCGCGGGCCT GGTGGCCATG GCGACAAGA TGGCGAGCCA  
 2751 CATCTCGCGC GCGCTGTTC TCCCCCGAT CAAGCTCGAG TGCGAAAAA  
 55 2801 CGTTCACCAA GCTGCTGCTC ATCGCCAAGA AAAAGTACAT CGGCGTCATC  
 2851 TGCGGGGGCA AGATGCTCAT CAAGGGCGTG GATCTGGTGC GCAAAAACAA

2901 CTGCGCGTTT ATCAACCGCA CCTCCAGGGC CCTGGTCGAC CTGCTGTTTT  
 2951 ACGACGATAC CGTATCCGGA GCGGCCGCCG CGTTAGCCGA GCGCCCCGCA  
 5 3001 GAGGAGTGGC TGGCGCGACC CCTGCCCCGAG GGA CTGCAGG CGTTCGGGGC  
 3051 CGTCCTCGTA GACGCCCATC GGCGCATCAC CGACCCGGAG AGGGACATCC  
 3101 AGGACTTTGT CCTCACCGCC GAACTGAGCA GACACCCGCG CGCGTACACC  
 10 3151 AACAAGCGCC TGGCCACCT GACGGTGTAT TACAAGCTCA TGGCCCCGCC  
 3201 CGCGCAGGTC CCGTCCATCA AGGACCGGAT CCCGTACGTG ATCGTGGCCC  
 15 3251 AGACCCGCGA GGTAGAGGAG ACGGTCGCGC GGCTGGCCGC CCTCCGCGAG  
 3301 CTAGACGCCG CCGCCCCAGG GGACGAGCCC GCGCCCCCAG CGGCCCTGCC  
 3351 CTCCCCGGCC AAGCGCCCCC GGGAGACGCC GTCGCATGCC GACCCCCCGG  
 20 3401 GAGGCGCGTC CAAGCCCCGC AAGCTGCTGG TGTCCGAGCT GGC GGAGGAT  
 3451 CCCGGGTACG CCATCGCCCG GGGCGTTCCG CTCAACACGG ACTATTACTT  
 25 3501 CTCGCACCTG CTGGGGGCGG CCTGCGTGAC GTTCAAGGCC CTGTTTGGAA  
 3551 ATAACGCCAA GATCACCGAG AGTCTGTAA AGAGGTTTAT TCCCGAGACG  
 3601 TGGCACCCCC CGGACGACGT GGCCGCGCGG CTCAGGGCCG CGGGGTTCGG  
 30 3651 GCCGGCGGGG GCCGGCGCTA CGGCGGAGGA AACTCGTCGA ATGTTGCATA  
 3701 GAGCCTTTGA TACTCTAGCA TGA  
 35



**SEQ.ID.NO. 4** Amino acid sequence of DNA polymerase for HSV2-186-M1

5       1 MFCAAGGPAS PGGKSAARAA SGFFAPHNPR GATQTAPPPC RRQNFYNPHL  
       51 AQTGTQPKAP GPAQRHTYYS ECDEFRIAP RSLDEDAPAE QRTGVHDGRL  
       101 RRAPKVYCGG DERDVLRVGP EGFWRRLRL WGGADHAPEG FDPTVTVFHV  
 10       151 YDILEHVEHA YSMRAAQLHE RFMDAITPAG TVITLLGLTP EGHRAVHVY  
       201 GTRQYFYMNK AEVDRHLQCR APRDLCERLA AALRESPGAS FRGISADHFE  
       251 AEVVERADVY YYETRPTLYY RVFVRSGRAL AYLCDNFCEPA IRKYEGGVDA  
 15       301 TTRFILDNPG FVTFGWYRLK PGRGNAPAQ RPPTAFGTSS DVEFNCTADN  
       351 LAVEGAMCDL PAYKLMCFDI ECKAGGEDEL AFPVAERPED LVIQISCLLY  
 20       401 DLSTTALEHI LLFSLGSCDL PESHLSDLAS RGLPAPVVLE FDSEFEMLLA  
       451 FMTFVKQYGP EFVTGYNIN FDWPFVLTKL TEIYKVPLDG YGRMNNGRGVF  
       501 RVWDIGQSHF QKRSEKIVNG MVNIDMYGII TDKVKLSSYK LNAVAEAVLK  
 25       551 DKKKDLSDYD IPAYYASGPA QRGVIGEYCV QDSLLVGQLF FKFLPHLELS  
       601 AVARLAGINI TRTIYDGQOI RVFTCLLRLA GQKGFILPDT QGRFRGLDKE  
 30       651 APKRPVPRG EGERPGDGNG DEDKDDDEDG DEDGDREEV ARETGGRHVG  
       701 YQGARVLDPT SGFHVDPVVV FDFASLYPSI IQAHNLCFST LSLRPEAVAH  
       751 LEARDYLEI EVGGRRLLFFV KAHVRESLLS ILLRDWLAMR KQIRSRIQPS  
 35       801 PPEEAVLLDK QQAIAKVVCN SVYGFTGAQH GLLPCLHVAA TVTTIGREML  
       851 LATRAYVHAR WAEFDQLLAD FPEAAGMRAP GPYSMRIYG DTDSIFVLCR  
 40       901 GLTAAGLVAM GDKMASHIS ALFLPIKLE CEKTFTKLLL IAKKKYIGVI  
       951 CGGKMLIKGV DLVRKNNCAF INRTSRALVD LLFYDDTVSG AAAALAERPA  
       1001 EEWLARPLPE GLQAFGAVLV DAHRRITDPE RDIQDFVLTA ELSRHPRAYT  
       1051 NKRLAHLTVY YKLMARRAQV PSIKDRIPYV IVAQTREVEE TVARLAALRE  
       1101 LDAAAPGDEP APPAALPSA KRPRETSHA DPPGGASKPR KLLVSELAED  
 50       1151 PGYAIARGVP LNTDYYFSHL LGAACVTFKA LFGNNAKITE SLLKRFIPET  
       1201 WHPPDDVAAR LRAAGFGPAG AGATAEETRR MLHRAFDTLA \*  
 55

**SEQ.ID.NO. 5**      DNA sequence of DNA polymerase gene for HSV1-KOS-M1

1 ATGTTTTCCG GTGGCGGCGG CCCGCTGTCC CCCGGAGGAA AGTCGGCGGC  
 5 51 CAGGGCGGCG TCCGGGTTTT TTGCGCCCGC CGGCCCTCGC GGAGCCGGCC  
 101 GGGGACCCCC GCCTTGTTTG AGGCAAACT TTTACAACCC CTACCTCGCC  
 151 CCAGTCGGGA CGCAACAGAA GCCGACCGGG CCAACCCAGC GCCATACGTA  
 10 201 CTATAGCGAA TGCATGAAT TTCGATTCAT CGCCCCGCGG GTGCTGGACG  
 251 AGGATGCCCC CCCGGAGAAG CGCGCCGGGG TGCACGACGG TCACCTCAAG  
 15 301 CGCGCCCCCA AGGTGTACTG CGGGGGGGAC GAGCGCGACG TCCTCCGCGT  
 351 CGGGTCGGGC GGCTTCTGGC CGCGGCGCTC GCGCCTGTGG GGCGGCGTGG  
 401 ACCACGCCCC GCGGGGGTTC AACCCACCG TCACCGTCTT TCACGTGTAC  
 20 451 GACATCCTGG AGAACGTGGA GCACGCGTAC GGCATGCGCG CGGCCCAGTT  
 501 CCACGCGCGG TTTATGGACG CCATCACACC GACGGGGACC GTCATCACGC  
 25 551 TCCTGGGCCT GACTCCGGAA GGCCACCGGG TGGCCGTTCA CGTTTACGGC  
 601 ACGCGGCAGT ACTTTTACAT GAACAAGGAG GAGGTTGACA GGCACCTACA  
 651 ATGCCGCGCC CCACGAGATC TCTGCGAGCG CATGGCCGCG GCCCTGCGCG  
 30 701 AGTCCCCGGG CGCGTCGTTT CGCGGCATCT CCGCGGACCA CTTCGAGGGC  
 751 GAGGTGGTGG AGCGCACCGA CGTGTACTAC TACGAGACGC GCCCCGCTCT  
 35 801 GTTTTACCGC GTCTACGTCC GAAGCGGGCG CGTGCTGTCG TACCTGTGCG  
 851 ACAACTTCTG CCCGGCCATC AAGAAGTACG AGGGTGGGGT CGACGCCACC  
 901 ACCCGGTTCA TCCTGGACAA CCCCGGGTTC GTCACCTTCG GCTGGTACCG  
 40 951 TCTCAAACCG GGCCGGAACA ACACGCTAGC CCAGCCGCGG GCCCCGATGG  
 1001 CCTTCGGGAC ATCCAGCGAC GTCGAGTTTA ACTGTACGGC GGACAACCTG  
 45 1051 GCCATCGAGG GGGGCATGAG CGACCTACCG GCATACAAGC TCATGTGCTT  
 1101 CGATATCGAA TGCAAGGCGG GGGGGGAGGA CGAGCTGGCC TTTCCGGTGG  
 1151 CCGGGCACCC GGAGGACCTG GTTATTCAGA TATCCTGTCT GCTCTACGAC  
 50 1201 CTGTCCACCA CCGCCCTGGA GCACGTCCTC CTGTTTTCGC TCGGTTCTTG  
 1251 CGACCTCCCC GAATCCCACC TGAACGAGCT GCGGCCAGG GGCCTGCCCA  
 55 1301 CGCCCGTGGT TCTGGAATTC GACAGCGAAT TCGAGATGCT GTTGGCCTTC  
 1351 ATGACCCTTG TGAAACAGTA CGGCCCCGAG TTCGTGACCG GGTACAACAT  
 1401 CATCAACTTC GACTGGCCCT TCTTGCTGGC CAAGTTGACG GACATTTACA

1451 AGGTCCCCCT GGACGGGTAC GGCCGCATGA ACGGCCGGGG CGTGTTTCGC  
 1501 GTGTGGGACA TAGGCCAGAG CCACTTCCAG AAGCGCAGCA AGATAAAGGT  
 5 1551 GAACGGCATG GTGAACATCG ACATGTACGG GATCATAACC GACAAGATCA  
 1601 AGCTCTCGAG CTACAAGCTC AACGCCGTGG CCGAAGCCGT CCTGAAGGAC  
 10 1651 AAGAAGAAGG ACCTGAGCTA TCGCGACATC CCCGCCTACT ACGCCGCCGG  
 1701 GCCCGCGCAA CGCGGGGTGA TCGGCGAGTA CTGCATACAG GATTCCCTGC  
 1751 TGGTGGGCCA GCTGTTTTTT AAGTTTTTGC CCCATCTGGA GCTCTCGGCC  
 15 1801 GTCGCGCGCT TGGCGGGTAT TAACATCACC CGCACCATCT ACGACGGCCA  
 1851 GCAGATCCGC GTCTTTACGT GCCTGCTGCG CCTGGCCGAC CAGAAGGGCT  
 20 1901 TTATTCTGCC GGACACCCAG GGGCGATTTA GGGGCGCCGG GGGGGAGGCG  
 1951 CCCAAGCGTC CGGCCGCAGC CCGGGAGGAC GAGGAGCGGC CAGAGGAGGA  
 2001 GGGGGAGGAC GAGGACGAAC GCGAGGAGGG CGGGGGCGAG CGGGAGCCGG  
 25 2051 AGGGCGCGCG GGAGACCGCC GGCCGGCACG TGGGGTACCA GGGGGCCAGG  
 2101 GTCCTTGACC CCACTTCCGG GTTTCACGTG AACCCCGTGG TGGTGTTCTGA  
 30 2151 CTTTGCCAGC CTGTACCCCA GCATCATCCA GGCCACAAC CTGTGCTTCA  
 2201 GCACGCTCTC CCTGAGGGCC GACGCAGTGG CGCACCTGGA GGCGGGCAAG  
 2251 GACTACCTGG AGATCGAGGT GGGGGGGCGA CGGCTGTTCT TCGTCAAGGC  
 35 2301 TCACGTGCGA GAGAGCCTCC TCAGCATCCT CCTGCGGGAC TGGCTCGCCA  
 2351 TGCGAAAGCA GATCCGCTCG CGGATTCCCC AGAGCAGCCC CGAGGAGGCC  
 40 2401 GTGCTCCTGG ACAAGCAGCA GGCCGCCATC AAGGTCGTGT GTAACTCGGT  
 2451 GTACGGGTTC ACGGGAGCGC AGCACGGA CTGCGCGTGC CTGCACGTTG  
 2501 CCGCGACGGT GACGACCATC GGCCGCGAGA TGCTGCTCGC GACCCGCGAG  
 45 2551 TACGTCCACG CGCGCTGGGC GGCCTTCGAA CAGCTCCTGG CCGATTTCCT  
 2601 GGAGGCGGCC GACATGCGCG CCCCCGGGCC CTATTCCATG CGCATCATCT  
 50 2651 ACGGGGACAC GGACTCCATA TTTGTGCTGT GCCGCGGCCT CACGGCCGCC  
 2701 GGGCTGACGG CCATGGGCGA CAAGATGGCG AGCCACATCT CGCGCGCGCT  
 2751 GTTTCTGCCC CCCATCAAAC TCGAGTGCGA AAAGACGTTC ACCAAGCTGC  
 55 2801 TGCTGATCGC CAAGAAAAAG TACATCGGCG TCATCTACGG GGGTAAGATG  
 2851 CTCATCAAGG GCGTGGATCT GGTGCGCAAA AACAACTGCG CGTTTATCAA

2901 CCGCACCTCC AGGGCCCTGG TCGACCTGCT GTTTTACGAC GATACCGTAT  
2951 CCGGAGCGGC CGCCGCGTTA GCCGAGCGCC CCGCAGAGGA GTGGCTGGCG  
5 3001 CGACCCCTGC CCGAGGGACT GCAGGCGTTC GGGGCCGTCC TCGTAGACGC  
3051 CCATCGGCGC ATCACCGACC CGGAGAGGGA CATCCAGGAC TTTGTCCTCA  
3101 CCGCCGA ACT GAGCAGACAC CCGCGCGCGT ACACCAACAA GCGCCTGGCC  
10 3151 CACCTGACGG TGTATTACAA GCTCATGGCC CGCCGCGCGC AGGTCCCCTC  
3201 CATCAAGGAC CGGATCCCGT ACGTGATCGT GGCCCAGACC CGCGAGGTAG  
15 3251 AGGAGACGGT CGCGCGGCTG GCCGCCCTCC GCGAGCTAGA CGCCGCCGCC  
3301 CCAGGGGACG AGCCCGCCCC CCCC GCGGCC CTGCCCTCCC CGGCCAAGCG  
3351 CCCCCGGGAG ACGCCGTCGC ATGCCGACCC CCCGGGAGGC GCGTCCAAGC  
20 3401 CCCGCAAGCT GCTGGTGTCC GAGCTGGCCG AGGATCCCGC ATACGCCATT  
3451 GCCCACGGCG TCGCCCTGAA CACGGACTAT TACTTCTCCC ACCTGTTGGG  
25 3501 GCGGGCGTGC GTGACATTCA AGGCCCTGTT TGGGAATAAC GCCAAGATCA  
3551 CCGAGAGTCT GTTAAAAAGG TTTATTCCCG AAGTGTGGCA CCCCCCGGAC  
3601 GACGTGGCCG CGCGGCTCCG GGCCGCAGGG TTCGGGGCGG TGGGTGCCGG  
30 3651 CGCTACGGCG GAGGAACTC GTCGAATGTT GCATAGAGCC TTTGATACTC  
3701 TAGCATGA

35

**SEQ.ID.NO. 6** Amino acid sequence of DNA polymerase for HSV1-KOS-M1

1 MFSGGGGPLS PGGKSAARAA SGFFAPAGPR GAGRGPPPCL RQNFYNPYLA  
 5 51 PVGTQQKPTG PTQRHTYYSE CDEFRIAPR VLDEDAPEK RAGVHDGHLK  
 101 RAPKVYCGGD ERDVLRVGSG GFWPRRSRLW GGVDHAPAGF NPTVTVFHVY  
 10 151 DILENVEHAY GMRAAQFHAR FMDAITPTGT VITLLGLTPE GHRVAVHVY  
 201 TRQYFYMNKE EVDRHLQCRA PRDLCERMAA ALRESPGASF RGISADHFEA  
 251 EVVERTDVYY YETRPALFYR VYVRSGRVLS YLCDNFCPAI KKYEGGVDAT  
 15 301 TRFILDNPGF VTFGWYRLKP GRNNTLAQPR APMAFGTSSD VEFNCTADNL  
 351 AIEGGMSDLP AYKLMCFDIE CKAGGEDELA FPVAGHPEDL VIQISCLLYD  
 20 401 LSTTALEHVL LFSLGSCDLP ESHLNELAAR GLTPVVLEF DSEFEMLLAF  
 451 MTLVKQYGPE FVTGYNIINF DWPFLAKLT DIYKVPLDGY GRMNGRGVFR  
 501 VWDIGQSHFQ KRSKIKVNGM VNIDMYGIIT DKIKLSSYKL NAVAEAVLKD  
 25 551 KKKDLSYRDI PAYYAAGPAQ RGVIGEYCIQ DSLLVGQLFF KFLPHLELSA  
 601 VARLAGINIT RTIYDGQQIR VFTCLRLAD QKGFILPDTQ GRFRGAGGEA  
 30 651 PKRPAAARED EERPEEEGED EDEREEGGGE REPEGARETA GRHVGYYQGAR  
 701 VLDPTSGFHV NPVVVFDFAS LYPSIIQAHN LCFSTLSLRA DAVAHLEAGK  
 751 DYLEIEVGGR RLFFVKAHVR ESLLSILLRD WLAMRKQIRS RIPQSSPEEA  
 35 801 VLLDKQAAI KVV CNSVYGF TGAQHGLLPC LHVAATVTTI GREMLLATRE  
 851 YVHARWAAFE QLLADFPEAA DMRAPGPYSM RIYGD TDSI FVLCRGLTAA  
 40 901 GLTAMGDKMA SHISRALFLP PIKLECEKTF TKLLLIAKKK YIGVIYGGKM  
 951 LIKGVDLVRK NNCAFINRTS RALVDLLFYD DTVSGAAAAL AERPAAEWLA  
 1001 RPLPEGLQAF GAVLVDAHRR ITDPERDIQD FVLTAELSRH PRAYTNKRLA  
 45 1051 HLTVYYKLMA RRAQVPSIKD RPYVIVAQT REVEETVARL AALRELDAAA  
 1101 PGDEPAPPAA LPSPAKRPRE TP SHADPPGG ASKPRKLLVS ELAEDPAYAI  
 50 1151 AHGVALNTDY YFSHLLGAAC VTFKALFGNN AKITESLLKR FIPEVWHPPD  
 1201 DVAARLRAAG FGAVGAGATA EETRRMLHRA FDTLA\*

**SEQ.ID.NO. 7**      DNA sequence of HSV polymerase gene for HSV1-F-M1

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5      1  ATGTTTTCCG GTGGCGGCGG CCCGCTGTCC CCCGGAGGAA AGTCGGCGGC
      51  CAGGGCGGCG TCCGGGTTTT TTGCGCCCGC CGGCCCTCGC GGAGCCGGCC
     101  GGGGACCCCC GCCTTGCTTG AGGCAAAACT TTTACAACCC CTACCTCGCC
10     151  CCAGTCGGGA CGCAACAGAA GCCGACCGGG CCAACCCAGC GCCATACGTA
      201  CTATAGCGAA TCGATGAAT TTCGATTCAT CGCCCCGCGG GTGCTGGACG
      251  AGGATGCCCC CCCGGAGAAG CGCGCCGGGG TGCACGACGG TCACCTCAAG
15     301  CGCGCCCCCA AGGTGTACTG CGGGGGGGAC GAGCGCGACG TCC'TCCGCGT
      351  CGGGTCGGGC GGCTTCTGGC CGCGGCGCTC GCGCCTGTGG GCGGCGTGG
20     401  ACCACGCCCC GCGGGGGTTC AACCACACCG TCACCGTCTT TCACGTGTAC
      451  GACATCCTGG AGAACGTGGA GCACGCGTAC GGCATGCGCG CGGCCCAGTT
      501  CCACGCGCGG TTTATGGACG CCATCACACC GACGGGGACC GTCATCACGC
25     551  TCCTGGGCCT GACTCCGGA AAGCCACCGG TGGCCGTTC ACGTTTACGGC
      601  ACGCGGCAGT ACTTTTACAT GAACAAGGAG GAGGTCGACA GGCACCTACA
30     651  ATGCCGCGCC CCACGAGATC TCTGCGAGCG CATGGCCGCG GCCCTGCGCG
      701  AGTCCCCGGG CGCGTCGTTC CGCGGCATTT CCGCGGACCA CTTCGAGGCG
      751  GAGGTGGTGG AGCGCACCGA CGTGTACTION TACGAGACGC GCCCCGCTCT
35     801  GTTTTACCGC GTCTACGTCC GAAGCGGGCG CGTGCTGTG TACCTGTGCG
      851  ACAACTTCTG CCCGGCCATC AAGAAGTACG AGGGTGGGGT CGACGCCACC
40     901  ACCCGGTTCA TCCTGGACAA CCCCAGGTTC GTCACCTTCG GCTGGTACCG
      951  TCTCAAACCG GGCCGGAACA ACACGCTAGC CCAGCCGCGG GCCCCGATGG
     1001  CCTTCGGGAC ATCCAGCGAC GTCGAGTTTA ACTGTACGGC GGACAACCTG
45     1051  GCCATCGAGG GGGGCATGAG CGACCTACCG GCATACAAGC TCATGTGCTT
     1101  CGATATCGAA TGCAAGGCGG GGGGGGAGGA CGAGCTGGCC TTTCCGGTGG
50     1151  CCGGGCACCC GGAGGACCTG GTCATCCAGA TATCCTGTCT GCTCTACGAC
     1201  CTGTCCACCA CCGCCCTGGA GCACGTCCTC CTGTTTTTCG TCGGTTCCCTG
     1251  CGACCTCCCC GAATCCCACC TGAACGAGCT GGCGGCCAGG GGCCTGCCCA
55     1301  CGCCCGTGGT TCTGGAATTC GACAGCGAAT TCGAGATGCT GTTGGCCTTC
     1351  ATGACCCTTG TGAAACAGTA CGGCCCCGAG TTCGTGACCG GGTACAACAT
60     1401  CATCAACTTC GACTGGCCCT TCTTGCTGGC CAAGCTGACG GACATTTACA
     1451  AAGTCCCCCT GGACGGGTAC GGCCGCATGA ACGGCCGGGG CGTGTTTTCG
     1501  GTGTGGGACA TAGGCCAGAG CCACTTCCAG AAGCGCAGCA AGATAAAGGT

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1551 GAACGGCATG GTGAACATCG ACATGTACGG GATTATAACC GACAAGATCA  
 1601 AGCTCTCGAG CTACAAGCTC AACGCCGTGG CCGAAGCCGT CCTGAAGGAC  
 5 1651 AAGAAGAAAG ACCTGAGCTA TCGCGACATC CCCGCCTACT ACGCCGCCGG  
 1701 GCCCGCGCAA CGCGGGGTGA TCGCGAGTA CTGCATACAG GATTCCCTGC  
 10 1751 TGGTGGGCCA GCTGTTTTTTT AAGTTTTTGC CCCATCTGGA GCTCTCGGCC  
 1801 GTCGCGCGCT TGGCGGGTAT TAACATCACC CGCACCATCT ACGACGGCCA  
 1851 GCAGATCCGC GTCTTTTACGT GCGTGC'TGCG CCTGGCCGAC CAGAAGGGCT  
 15 1901 TTATTC'TGCC GGACACCCAG GGGCGATTTA GGGGCGGCGG GGGGGAGGCG  
 1951 CCCAAGCGTC CGGCCGCAGC CCGGGAGGAC GAGGAGCGGC CAGAGGAGGA  
 20 2001 GGGGGAGGAC GAGGACGAAC GCGAGGAGGG CGGGGGCGAG CGGGAGCCGG  
 2051 AGGGCGCGCG GGAGACCGCC GGCCGGCACG TGGGGTACCA GGGGGCCAGG  
 2101 GTCCTTGACC CCACTTCCGG GTTTCATGTG AACCCCGTGG TGGTGTTCGA  
 25 2151 CTTTGCCAGC CTGTACCCCA GCATCATCCA GGCCACAAC CTGTGCTTCA  
 2201 GCACGCTCTC CCTGAGGGCC GACGCAGTGG CGCACCTGGA GGCGGGCAAG  
 30 2251 GACTACCTGG AGATCGAGGT GGGGGGGCGA CGGCTGTTCT TCGTCAAGGC  
 2301 TCACGTGCGA GAGAGCCTCC TCAGCATCCT CCTGCGGGAC TGGCTCGCCA  
 2351 TGCGAAAGCA GATCCGCTCG CGGATTCCCC AGAGCAGCCC CGAGGAGGCC  
 35 2401 GTGCTCCTGG ACAAGCAGCA GGCCGCCATC AAGGTCGTGT GTAACTCGGT  
 2451 TTACGGGTTC ACGGGAGCGC AGCACGGACT CCTGCCGTGC CTGCACGTTG  
 40 2501 CCGCGACGGT GACGACCATC GGCCGCGAGA TGCTGCTCGC GACCCGCGAG  
 2551 TACGTCCACG CGCGCTGGGC GGCCTTCGAA CAGCTCCTGG CCGATTTCCC  
 2601 GGAGGCGGCC GACATGCGCG CCCCCGGGCC CTATTCCATG CGCATCATCT  
 45 2651 ACGGGGACAC GGACTCCATC TTTGTGCTGT GCCGCGGCCT CACGGCCGCC  
 2701 GGGCTGACGG CCGTGGGCGA CAAGATGGCG AGCCACATCT CGCGCGCGCT  
 50 2751 GTTTC'TGTCC CCCATCAAAC TCGAGTGCGA AAAGACG'TTC ACCAAGCTGC  
 2801 TGCTGATCGC CAAGAAAAAG TACATCGGCG TCATCTACGG GGGTAAGATG  
 2851 CTCATCAAGG GCGTGGATCT GGTGCGCAAA AACAAC'TGCG CG'TTTATCAA  
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 2951 CCGGAGCGGC CGCCGCGTTA GCCGAGCGCC CCGCAGAGGA GTGGCTGGCG  
 60 3001 CGACCCCTGC CCGAGGGACT GCAGGCGTTC GGGGCCGTCC TCGTAGACGC  
 3051 CCATCGGCGC ATCACCGACC CGGAGAGGGA CATCCAGGAC TTTGTCTCTCA  
 3101 CCGCCGA'ACT GAGCAGACAC CCGCGCGCGT ACACCAACAA GCGCCTGGCC  
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	3151	CACCTGACGG	TGTATTACAA	GTCATGGCC	CGCCGCGCGC	AGGTCCCCGTC
	3201	CATCAAGGAC	CGGATCCCCGT	ACGTGATCGT	GGCCCAGACC	CGCGAGGTAG
5	3251	AGGAGACGGT	CGCGCGGCTG	GCCGCCCTCC	GCGAGCTCGA	CGCCGCCCGCC
	3301	CCAGGGGACG	AGCCCGCCCC	CCCCGCGGCC	CTGCCCTCCC	CGGCCAAGCG
	3351	CCCCCGGGAG	ACGCCGTTGC	ATGCCGACCC	CCCGGGAGGC	GCGTCCAAGC
10	3401	CCCGCAAGCT	GCTGGTGTCC	GAGCTGGCCG	AGGATCCCCG	ATACGCCATT
	3451	GCCCACGGCG	TCGCCCTGAA	CACGGACTAT	TACTTCTCCC	ACCTGTTGGG
15	3501	GGCGGCGTGC	GTGACATTCA	AGGCCCTGTT	TGGGAATAAC	GCCAAGATCA
	3551	CCGAGAGTCT	GTTAAAAAGG	TTTATTCCCG	AAGTGTGGCA	CCCCCGGAC
	3601	GACGTGGCCG	CGCGGCTCCG	GGCCGCAGGG	TTCGGGGCGG	TGGGTGCCGG
20	3651	CGCTACGGCG	GAGGAAACTC	GTCGAATGTT	GCATAGAGCC	TTTGATACTC
	3701	TAGCATGA				



**SEQ.ID.NO. 8**      Amino acid sequence of DNA polymerase for HSV1-F-M1

1 MFSGGGGPLS PGGKSAARAA SGFFAPAGPR GAGRGPPPCL RQNFYNPYLA  
 5 51 PVGTQQKPTG PTQRHTYYSE CDEFRIAPR VLDEDAPEK RAGVHDGHLK  
 101 RAPKVYCGGD ERDVLRVGSG GFWPRRSRLW GGVDHAPAGF NPTVTVFHVY  
 151 DILENVEHAY GMRAAQFHAR FMDAITPTGT VITLLGLTPE GHRVAVHVY  
 10 201 TRQYFYMNKE EVDRHLQCRA PRDLCERMAA ALRESPGASF RGISADHFEA  
 251 EVVERTDVYY YETRPALFYR VYVRSGRVLS YLCDNFCPAI KKYEGGV DAT  
 15 301 TRFILDNPGF VTFGWYRLKP GRNNTLAQPR APMAFGTSSD VEFNCTADNL  
 351 AIEGGMSDLP AYKLMCFDIE CKAGGEDELA FPVAGHPEDL VIQISCLLYD  
 401 LSTTALEHVL LPSLGSCDLP ESHLNELAAR GLPTPVVLEF DSEFEMLLAF  
 20 451 MTLVKQYGPE FVTGYNIINF DWPFLAKLT DIYKVPLDGY GRMN GRGVFR  
 501 VWDIGQSHFQ KRSKIKVNGM VNIDMYGIIT DKIKLSSYKL NAVAEAVLKD  
 25 551 KKKDLSYRDI PAYYAAGPAQ RGVIGEYCIQ DSLLVGQLFF KFLPHLELSA  
 601 VARLAGINIT RTIYDGQQIR VFTCLRLAD QKGFILPDTQ GRFRGGGGEA  
 651 PKRPAAARED EERPEEEGED EDEREEGGGE REPEGARETA GRHVGYQGAR  
 30 701 VLDPTSGFHV NPVVVDFAS LYPSIIQAHN LCFSTLSLRA DAVAHLEAGK  
 751 DYLEIEVGGR RLFFVKAHVR ESLLSILLRD WLAMRKQIRS RIPQSSPEEA  
 35 801 VLLDKQAAI KVCNSVYGF TGAQHGLLPC LHVAATVTI GREMLLATRE  
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 901 GLTAVGDKMA SHISRALFLS PIKLECEKTF TKLLLIAKKK YIGVIYGGKM  
 40 951 LIKGVDLVRK NNCAFINRTS RALVDLLFYD DTVSGAAAAL AERPAEEWLA  
 1001 RPLPEGLQAF GAVLVDAHRR ITDPERDIQD FVLTAELSRH PRAYTNKRLA  
 45 1051 HLTVYYKLMA RRAQVPSIKD RPYVIVAQT REVEETVARL AALRELDAAA  
 1101 PGDEPAPPAA LPSPAKRPRE TPLHADPPGG ASKPRKLLVS ELAEDPAYAI  
 1151 AHGVALNTDY YFSHLLGAAC VTFKALFGNN AKITESLLKR FIPEVWHPPD  
 50 1201 DVAARLRAAG FGAVGAGATA EETRRMLHRA FDTLA\*

**SEQ.ID.NO. 9**      DNA sequence of HSV polymerase gene for HSV1-DJL-M1

1 ATGTTTTCCG GTGGCGGCGG CCCGCTGTCC CCCGGAGGAA AGTCGGCGGC  
 5 51 CAGGGCGGCG TCCGGGTTTT TTGCGCCCGC CGGCCCTCGC GGAGCCGGCC  
 101 GGGGACCCCC GCCTTGTTTG AGGCAAACT TTTACAACCC CTACCTCGCC  
 151 CCAGTCGGGA CGCAACAGAA GCCGACCGGG CCAACCCAGC GCCATACGTA  
 10 201 CTATAGCGAA TGCATGAAT TTCGATTCAT CGCCCCGCGG GTGCTGGACG  
 251 AGGATGCCCC CCCGGAGAAG CGCGCCGGGG TGCACGACGG TCACCTCAAG  
 15 301 CGCGCCCCCA AGGTGTACTG CGGGGGGGAC GAGCGCGACG TCCTCCGCGT  
 351 CGGGTCGGGC GGCTTCTGGC CGCGGCGCTC GCGCCTGTGG GGC GGCGTGG  
 401 ACCACGCCCC GCGGGGGTTC AACCCACCG TCACCGTCTT TCACGTGTAT  
 20 451 GACATCCTGG AGAACGTGGA GCACGCGTAC GGCATGCGCG CGGCCAGTT  
 501 CCACGCGCGG TTTATGGACG CCATCACACC GACGGGGACC GTCATCACGC  
 25 551 TCCTGGGCCT GACTCCGGAA GGCCACCGGG TGGCCGTTCA CGTTTACGGC  
 601 ACGCGGCAGT ACTTTTACAT GAACAAGGAG GAGGTTGACA GGCACCTACA  
 651 ATGCCGCGCC CCACGAGATC TCTGCGAGCG CATGGCCGCG GCCCTGCGCG  
 30 701 AGTCCCCGGG CGCGTCGTTC CGCGGCATCT CCGCGGACCA CTTCGAGGCG  
 751 GAGGTGGTGG AGCGCACCGA CGTGTACTAC TACGAGACGC GCCCCGCTCT  
 35 801 GTTTTACCGC GTCTACGTCC GAAGCGGGCG CGTGCTGTCG TACCTGTGCG  
 851 ACAACTTCTG CCCGGCCATC AAGAAGTACG AGGGTGGGGT CGACGCCACC  
 901 ACCCGGTTCA TCCTGGACAA CCCCGGGTTC GTCACCTTCG GCTGGTACCG  
 40 951 TCTCAAACCG GGCCGGAACA ACACGCTAGC CCAGCCGCGG GCCCCGATGG  
 1001 CCTTCGGGAC ATCCAGCGAT GTCGAGTTTA ACTGTACGGC GGACAACCTG  
 45 1051 GCCATCGAGG GGGGCATGAG CGACCTACCG GCATACAAGC TCATGTGCTT  
 1101 CGATATCGAA TGCAAGGCGG GGGGGGAGGA CGAGCTGGCC TTTCCGGTGG  
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 50 1201 CTGTCCACCA CCGCCCTGGA GCACGTCCTC CTGTTTTCGC TCGGTTCTTG  
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 55 1301 CGCCCGTGGT TCTGGAATTC GACAGCGAAT TCGAGATGCT GTTGGCCTTC  
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1401 AATCAACTTC GACTGGCCCT TCTTGCTGGC CAAGCTGACG GACATTTACA  
 1451 AGGTCCCCCT GGACGGGTAC GGCCGCATGA ACGGCCGGGG CGTGTTTCGC  
 5 1501 GTGTGGGACA TAGGCCAGAG CCACTTCCAG AAGCGCAGCA AGATAAAGGT  
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 1601 AGCTCTCGAG CTACAAGCTC AACGCCGTGG CCGAAGCCGT CCTGAAGGAC  
 10 1651 AAGAAGAAGG ACCTGAGCTA TCGCGACATC CCCACCTACT ACGCCGCCGG  
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 1751 TGGTGGGCCA GCTGTTTTTT AAGTTTTTGC CCCATCTGGA GCTCTCGGCC  
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 1851 GCAGATCCGC GTCTTTACGT GCCTGCTGCG CCTGGCCGAC CAGAAGGGCT  
 20 1901 TTATTCTGCC GGACACCCAG GGGCGATTTA GGGGCGCCGG GGGGGAGGCG  
 1951 CCCAAGCGTC CGGCCGCAGC CCGGGAGGAC GAGGAGCGGC CAGAGGAGGA  
 25 2001 GGGGGAGGAC GAGAACGAAC GCGAGGAGGG CGGGGGCGAG CGGGAGCCGG  
 2051 AGGGCGCGCG GGAGACCGCC GGCCGGCACG TGGGGTACCA GGGGGCCAGG  
 2101 GTCCTTGACC CCACTTCCGG GTTTCACGTG AACCCCGTGG TGGTGTTCGA  
 30 2151 CTTTGCCAGC CTGTACCCCA GCATCATCCA GGCCCACAAC CTGTGCTTCA  
 2201 GCACGCTCTC CCTGAGGGCC GACGCAGTGG CGCACCTGGA GCGGGGCAAG  
 35 2251 GACTACCTGG AGATCGAGGT GGGGGGGCGA CGGCTGTTCT TCGTCAAGGC  
 2301 TCACGTGCGA GAGAGCCTCC TCAGCATCCT CCTGCGGGAC TGGCTCGCCA  
 2351 TGCGAAAGCA GATCCGCTCG CGGATTCCCC AGAGCAGCCC CGAGGAGGCC  
 40 2401 GTGCTCCTGG ACAAGCAGCA GGCCGCCATC AAGGTCGTGT GTAACCTCGGT  
 2451 TTACGGGTTC ACGGGAGCGC AGCACGGACT CCTGCCGTGC CTGCACGTTG  
 45 2501 CCGCGACGGT GACGACCATC GGCCGCGAGA TGCTGCTCGC GACCCGCGAG  
 2551 TACGTCCACG CGCGCTGGGC GGCCTTCGAA CAGCTCCTGG CCGATTTCCT  
 2601 GGAGGCGGCC GACATGCGCG CCCCCGGGCC CTATTCCATG CGCATCATCT  
 50 2651 ACGGGGACAC GGA CTCCATA TTTGTGCTGT GCCGCGGCCT CACGGCCGCC  
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 55 2751 GTTTCTGCCC CCCATCAAAC TCGAGTGCGA AAAGACGTTT ACCAAGCTGC  
 2801 TGCTGATCGC CAAGAAAAAG TACATCGGCG TCATCTACGG GGGTAAGATG  
 2851 CTCATCAAGG GCGTGGATCT GGTGCGCAA AACAACTGCG CGTTTATCAA

2901 CCGCACCTCC AGGGCCCTGG TCGACCTGCT GTTTTACGAC GATACCGTAT  
2951 CCGGAGCGGC CGCCGCGTTA GCCGAGCGCC CCGCAGAGGA GTGGCTGGCG  
5 3001 CGACCCCTGC CCGAGGGACT GCAGGCGTTC GGGGCCGTCC TCGTAGACGC  
3051 CCATCGGCGC ATCACCGACC CGGAGAGGGA CATCCAGGAC TTTGTTCTCA  
10 3101 CCGCCGA ACT GAGCAGACAC CCGCGCGCGT ACACCAACAA GCGCCTGGCC  
3151 CACCTGACGG TGTATTACAA GCTCATGGCC CGCCGCGCGC AGGTCCCGTC  
3201 CATCAAGGAC CGGATCCCGT ACGTGATCGT GGCCCAGACC CGCGAGGTAG  
15 3251 AGGAGACGGT CGCGCGGCTG GCCGCCCTCC GCGAGCTAGA CGCCGCCGCC  
3301 CCAGGGGACG AGCCCGCCCC CCCC GCGGCC CTGCCCTCCC CGGCCAAGCG  
20 3351 CCCCCGGGAG ACGCCGTCGC CTGCCGACCC CCCGGGAGGC GCGTCCAAGC  
3401 CCCGCAAGCT GCTGGTGTCC GAGCTGGCCG AGGATCCCGC ATACGCCATT  
3451 GCCCACGGCG TCGCCCTGAA CACGGACTAT TACTTCTCCC ACCTGTTGGG  
25 3501 GGC GGCGTGC GTGACATTCA AGGCCCTGTT TGGGAATAAC GCCAAGATCA  
3551 CCGAGAGTCT GTTAAAAAGG TTTATTCCCG AAGTGTGGCA CCCCCGGAC  
30 3601 GACGTGGCCG CGCGGCTCCG GACCGCAGGG TTCGGGGCGG TGGGTGCCGG  
3651 CGCTACGGCG GAGGAACTC GTCGAATGTT GCATAGAGCC TTTGATACTC  
3701 TAGCATGA  
35

**SEQ.ID.NO. 10** Amino acid sequence of DNA polymerase for HSV1-DJL-M1

1 MFSGGGGPLS PGGKSAARAA SGFFAPAGPR GAGRGPPPCL RQNFYNPYLA  
 5 51 PVGTQQKPTG PTQRHTYYSE CDEFRIAPR VLDEDAPEK RAGVHDGHLK  
 101 RAPKVYCGGD ERDVLRVGSG GFWPRRSRLW GGVDHAPAGF NPTVTVFHVY  
 151 DILENVEHAY GMRAAQFHAR FMDAITPTGT VITLLGLTPE GHRVAVHVY  
 10 201 TRQYFYMNKE EVDRHLQCRA PRDLCERMAA ALRESPGASF RGISADHFEA  
 251 EVVERTDVYY YETRPALFYR VYVRSGRVLS YLCDNFCPAI KKYEGGV DAT  
 15 301 TRFILDNPGF VTFGWYRLKP GRNNTLAQPR APMAFGTSSD VEFNCTADNL  
 351 AIEGGMSDLP AYKLMCFDIE CKAGGEDELA FPVAGHPEDL VIQISCLLYD  
 401 LSTTALEHVL LFSLGSCDLP ESHLNELAAR GLPTPVVLEF DSEFEMLLAF  
 20 451 MTLVKQYGPE FVTGYNIN F DWPFLAKLT DIYKVPLDGY GRMNGRGVFR  
 501 VWDIGQSHFQ KRSKIKVNGM VNIDMYGIIT DKIKLSSYKL NAVA EAVLKD  
 25 551 KKKDLSYRDI PTYYAAGPAQ RGVIGEYCIQ DSLLVGQLFF KFLPHLELSA  
 601 VARLAGINIT RTIYDGQQIR VFTCLRLAD QKGFILPDTQ GRFRGAGGEA  
 651 PKRPAAARED EERPEEEGED ENERE EGGGE REPEGARETA GRHVGYQGAR  
 30 701 VLDPTSGFHV NPVVVFDFAS LYPSIIQAHN LCFSTLSLRA DAVAHLEAGK  
 751 DYLEIEVGGR RLFFVKAHVR ESLLSILLRD WLAMRKQIRS RIPQSSPEEA  
 35 801 VLLDKQQA AI KVCNSVYGF TGAQHGLLPC LHVAATVT TI GREMLLATRE  
 851 YVHARWAAFE QLLADFP EAA DMRAPGPYSM RIYGD TDSI FVLCRGLTAA  
 901 GLTAVGDKMA SHISRALFLP PIKLECEKTF TKLLLI AKKK YIGVIYGGKM  
 40 951 LIKGVDLVRK NNCAFINRTS RALVDLLFYD DTVSGAAAAL AERPAE EWLA  
 1001 RLPPEGLQAF GAVLVDAHRR ITDPERDIQD FVLTAELSRH PRAYTNKRLA  
 45 1051 HLTVYYKLMA RRAQVPSIKD RPYVIVAQT REVEETVARL AALRELDAAA  
 1101 PGDEPAPPAA LPSPAKRPRE TPSPADPPGG ASKPRKLLVS ELAEDPAYAI  
 1151 AHGVALNTDY YFSHLLGAAC VTFKALFGNN AKITESLLKR FIPEVWHPPD  
 50 1201 DVAARLRTAG FGAVGAGATA EETRRMLHRA FDTLA\*

**SEQ.ID.NO. 11**      DNA sequence of DNA polymerase gene for HMCV-AD169-M1

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1  ATGTTTTTCA ACCCGTATCT GAGCGGCGGC GTGACCGGCG GTGCGGTCGC
5  51  GGGTGGCCGG CGTCAGCGTT CGCAGCCCGG CTCCGCGCAG GGCTCGGGCA
    101 AGCGGCCGCC ACAGAAACAG TTTTTCGAGA TCGTGCCGCG AGGTGTCATG
    151 TTCGACGGTC AGACGGGGTT GATCAAGCAT AAGACGGGAC GGCTGCCTCT
10  201 CATGTTCTAT CGAGAGATTA AACATTTGTT GAGTCATGAC ATGGTTTGGC
    251 CGTGTCTTGT GCGCGAGACC CTGGTGGGTC GCGTGGTGGG ACCTATTCGT
    301 TTTCACACCT ACGATCAGAC GGACGCCGTG CTCTTCTTCG ACTCGCCCGA
15  351 AAACGTGTCG CCGCGCTATC GTCAGCATCT GGTGCCTTCG GGGAACGTGT
    401 TGCGTTTCTT CGGGGCCACA GAACACGGCT ACAGTATCTG CGTCAACGTT
20  451 TTCGGGCAGC GCAGCTACTT TTAAGTGAG TACAGCGACA CCGATAGGCT
    501 GCGTGAGGTC ATTGCCAGCG TGGGCGAACT AGTGCCCGAA CCGCGGACGC
    551 CATA CGCCGT GTCTGTCACG CCGGCCACCA AGACCTCCAT CTATGGGTAC
25  601 GGGACGCGAC CCGTGCCCGA TTTGCAGTGT GTGTCTATCA GCAACTGGAC
    651 CATGGCCAGA AAAATCGGCG AGTATCTGCT GGAGCAGGGT TTTCCCGTGT
30  701 ACGAGGTCCG TGTGGATCCG CTGACGCGTT TGGTCATCGA TCGGCGGATC
    751 ACCACGTTCG GCTGGTGCTC CGTGAATCGT TACGACTGGC GGCAGCAGGG
    801 TCGCGCGTCG ACTTGTGATA TCGAGGTAGA CTGCGATGTC TCTGACCTGG
35  851 TGGCTGTGCC CGACGACAGC TCGTGGCCGC GCTATCGATG CCTGTCCTTC
    901 GATATCGAGT GCATGAGCGG CGAGGGTGGT TTTCCCTGCG CCGAGAAGTC
40  951 CGATGACATT GTCATT CAGA TCTCGT GCGT GTGCTACGAG ACGGGGGGAA
    1001 ACACCGCCGT GGATCAGGGG ATCCCAAACG GGAACGATGG TCGGGGCTGC
45  1051 ACTTCGGAGG GTGTGATCTT TGGGCACTCG GGTCTTCATC TCTTTACGAT
    1101 CGGCACCTGC GGGCAGGTGG GCCCAGACGT GGACGTCTAC GAGTTCCTT
    1151 CCGAATACGA GCTGCTGCTG GGCTTTATGC TTTTCTTTCA ACGGTACGCG
50  1201 CCGGCCTTTG TGACCGGTTA CAACATCAAC TCTTTTGACT TGAAGTACAT
    1251 CCTCACGCGT CTCGAGTACC TGTATAAGGT GGAATCGCAG CGCTTCTGCA
55  1301 AGTTGCCTAC GGCAGAGGGC GGCCGTTTCT TTTTACACAG CCCC GCCGTG
    1351 GGTTTAAAGC GGCAGTACGC CGCCGCTTTT CCCTCGGCTT CTCACAACAA

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1401 TCCGGCCAGC ACGGCCGCCA CCAAGGTGTA TATTGCGGGT TCGGTGGTTA  
 1451 TCGACATGTA CCCTGTATGC ATGGCCAAGA CTAACTCGCC CAACTATAAG  
 5 1501 CTCAACACTA TGGCCGAGCT TTACCTGCGG CAACGCAAGG ATGACCTGTC  
 1551 TTACAAGGAC ATCCCGCGTT GTTTCGTGGC TAATGCCGAG GGCCGCGCCC  
 1601 AGGTAGGCCG TTAAGTCTCG CAGGACGCCG TATTGGTGCG CGATCTGTTC  
 10 1651 AACACCATTA ATTTTCACTA CGAGGCCGGG GCCATCGCGC GGCTGGCTAA  
 1701 AATTCCGTTG CGGCGTGTCA TCTTTGACGG ACAGCAGATC CGTATCTACA  
 1751 CCTCGCTGCT GGACGAGTGC GCCTGCCGCG ATTTTATCCT GCCCAACCAC  
 1801 TACAGCAAAG GTACGACGGT GCCCGAAACG AATAGCGTTG CTGTGTCACC  
 1851 TAACGCTGCT ATCATCTCTA CCGCCGCTGT GCCCGGCGAC GCGGGTTCTG  
 20 1901 TGGCGGCTAT GTTTCAGATG TCGCCGCCCT TGCAATCTGC GCCGTCCAGT  
 1951 CAGGACGGCG TTTCACCCGG CTCCGGCAGT AACAGTAGTA GCAGCGTCGG  
 2001 CGTTTTTCAGC GTCGGCTCCG GCAGTAGTGG CGGCGTCGGC GTTTCCAACG  
 2051 ACAATCACGG CGCCGGCGGT ACTGCGGCGG TTTCGTACCA GGGCGCCACG  
 2101 GTGTTTGAGC CCGAGGTGGG TTAAGTACAAC GACCCCGTGG CCGTGTTCTGA  
 30 2151 CTTTGCCAGC CTCTACCCTT CCATCATCAT GGCCACAAAC CTCTGCTACT  
 2201 CCACCCTGCT GGTGCCGGGT GGCAGTACC CTGTGGACCC CGCCGACGTA  
 2251 TACAGCGTCA CGCTAGAGAA CGGCGTGACC CACCGCTTTG TGCCTGCTTC  
 2301 GGTGCGCGTC TCGGTGCTCT CGGAAGTGT CAACAAGTGG GTTTCGCAGC  
 2351 GGCCTGCCGT GCGCGAATGC ATGCGCGAGT GTCAAGACCC TGTGCGCCGT  
 40 2401 ATGCTGCTCG ACAAGGAACA GATGGCGCTC AAAGTAACGT GCAACGCTTT  
 2451 CTACGGTTTT ACCGGCGCGC TGAACGGTAT GATGCCGTGT CTGCCCATCG  
 2501 CCGCCAGCAT CACGCGCATC GGTGCGGACA TGCTAGAGCG CACGGCGCGG  
 2551 TTCATCAAAG ACAACTTTTC AGAGCCGTGT TTTTGCACA ATTTTTTTAA  
 2601 TCAGGAAGAC TATGTAGTGG GAACGCGGGA GGGGGATTCG GAGGAGAGCA  
 50 2651 GCGCGTTACC GGAGGGGCTC GAAACATCGT CAGGGGGCTC GAACGAACGG  
 2701 CGGGTGGAGG CGCGGGTCAT CTACGGGGAC ACGGACAGCG TGTTTGTCGG  
 2751 CTTTCGTGGC CTGACGCCGC AGGCTCTGGT GGCCTGTGGG CCCAGCCTGG  
 2801 CGCACTACGT GACGGCCTGT CTTTTGTGG AGCCCGTCAA GCTGGAGTTT  
 2851 GAAAAGGTCT TCGTCTCTCT TATGATGATC TGCAAGAAAC GTTACATCGG

2901 CAAAGTGGAG GGC GCCTCGG GTCTGAGCAT GAAGGGCGTG GATCTGGTGC  
2951 GCAAGACGGC CTGCGAGTTC GTCAAGGGCG TCACGCGTGA CGTCCTCTCG  
5 3001 CTGCTCTTTG AGGATCGCGA GGTCTCGGAA GCAGCCGTGC GCCTGTCGCG  
3051 CCTCTCACTC GATGAAGTCA AGAAGTACGG CGTGCCACGC GGTTCCTGGC  
10 3101 GTATCTTACG CCGCTTGGTG CAGGCCCCGCG ACGATCTGTA CCTGCACCGT  
3151 GTGCGTGTCG AGGACCTGGT GCTTTCGTCG GTGCTCTCTA AGGACATCTC  
3201 GCTGTACCGT CAATCTAACC TGCCGCACAT TGCCGTCATT AAGCGATTGG  
15 3251 CGGCCCGTTC TGAGGAGCTA CCCTCGGTCG GGGATCGGGT CTTTTACGTT  
3301 CTGACGGCGC CCGGTGTCCG GACGGCGCCG CAGGGTTCCT CCGACAACGG  
20 3351 TGATTCTGTA ACCGCCGGCG TGGTTTCCCG GTCGGACGCG ATTGATGGCA  
3401 CGGACGACGA CGCTGACGGC GGC GGGGTAG AGGAGAGCAA CAGGAGAGGA  
3451 GGAGAGCCGG CAAAGAAGAG GGCGCGGAAA CCACCGTCGG CCGTGTGCAA  
25 3501 CTACGAGGTA GCCGAAGATC CGAGCTACGT GCGCGAGCAC GGCGTGCCCA  
3551 TTCACGCCGA CAAGTACTTT GAGCAGGTTC TCAAGGCTGT AACTAACGTG  
30 3601 CTGTCGCCCC TCTTTCCCGG CGGCGAAACC GCGCGCAAGG ACAAGTTTTT  
3651 GCACATGGTG CTGCCGCGGC GCTTGCACTT GGAGCCGGCT TTTCTGCCGT  
3701 ACAGTGTC AA GGCGCACGAA TGCTGTTGA  
35



**SEQ. ID. NO. 12      Amino acid sequence of DNA polymerase for HCMV-AD169-M1**

1 MFFNPYLSGG VTGGAVAGGR RQRSQPGSAQ GSGKRPPQKQ FLQIVPRGVM  
 5 51 FDGQTGLIKH KTGRLLPLMFY REIKHLLSHD MVWPCPWRET LVGRVVGPRI  
 101 FHTYDQTDV LFFDSPENVV PRYRQHLVPS GNVLRFFGAT EHGYSICVNV  
 10 151 FGQRSYFYCE YSDTDRLREV IASVGELVPE PRTPYAVSVT PATKTSIYGY  
 201 GTRPVPDLQC VSISNWTMAR KIGEYLLEQG FPVYEVRVDP LTRLVIDRRI  
 251 TTFGWCSVNR YDWRQQGRAS TCDIEVDCDV SDLVAVPDDS SWPRYRCLSF  
 15 301 DIECMSGEGG FPCAESDDI VIQISCVCYE TGGNTAVDQG IPNGNDGRGC  
 351 TSEGVIHGHS GLHLFTIGTC GQVGPDVDVY EFPSEYELLL GFMLFFQRYA  
 401 PAFVTGYNIN SFDLKYILTR LEYLYKVDSQ RFCKLPTAQG GRFFLHSPAV  
 451 GFKRQYAAAF PSASHNNPAS TAATKVYIAG SVVIDMYPVC MAKTNSPNYK  
 501 LNTMAELYLR QRKDDLSYKD IPRCFVANAE GRAQVGRYCL QDAVLVRDLF  
 25 551 NTINFHYEAG AIARLAKIPL RRVIFDGQOI RIYTSLLDEC ACRDFILPNH  
 601 YSKGTTVPET NSVAVSPNAA IISTAAPVGD AGSVAAMFQM SPPLQSAPSS  
 30 651 QDGVSPGSGS NSSSSVGVFS VSGSGSSGGVG VSNDNHGAGG TAAVSYQGAT  
 701 VFEPEVGYYN DPVAVDFAS LYPHIIMAHN LCYSTLLVPG GEYPVDPADV  
 751 YSVTLENGVT HRFVVRASRV SVLSELLNKW VSQRRVREC MRECQDPVRR  
 35 801 MLLDKEQMAL KVTCAFYGF TGALNGMMPC LPIAASITRI GRDMLERTAR  
 851 FIKDNFSEPC FLHNFFNQED YVVGTTREGDS EESSALPEGL ETSSGGSNER  
 40 901 RVEARVTYGD TDSVFVRFRG LTPQALVARG PSLAHYVTAC LFVEPVKLEF  
 951 EKVFSVSLMMI CKKRYIGKVE GASGLSMKGV DLVRKTACEF VKGVTRDVLS  
 1001 LLFEDREVSE AAVRLSRLSL DEVKKYGVPR GFWRILRRLV QARDDLYLHR  
 45 1051 VRVEDLVLS VLSKDISLYR QSNLPHIAVI KRLAARSEEL PSVGDRVFYV  
 1101 LTAPGVRTAP QGSSDNGDSV TAGVVSRSDA IDGTDDDADG GGVEESNRRG  
 1151 GEPAKKRARK PPSAVCNIEV AEDPSYVREH GVPIHADKYF EQVLKAVTNV  
 50 1201 LSPVFPGET ARKDKFLHMLV LPRRLHLEPA FLPYSVKAHE CC\*

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**Figure 6**  
**SEQ.ID.NO.13**      **Amino acid sequence of DNA polymerase for HCMV-AD169**

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5      1 MFFNPYLSGG VTGGAVAGGR RQRSQPGSAQ GSGKRPPQKQ FLQIVPRGVM
      51 FDGQTGLIKH KTGRLPLMFY REIKHLLSHD MVWPCPWRET LVGRVVGPIR
      101 FHTYDQTDV LFFDSPENV S PRYRQHLVPS GNVLRFFGAT EHGYSICVNV
10     151 FGQRSYFYCE YSDTDRLREV IASVGELVPE PRTPYAVSVT PATKTSIYGY
      201 GTRPVLDLQC VSISNWTMAR KIGEYLLEQG FPVYEVRVDP LTRLVIDRRI
      251 TTFGWCSVNR YDWRQQGRAS TCDIEVDCDV SDLVAVPDDS SWPRYRCLSF
15     301 DIECMSGEGG FPCAESDDI VIQISCVCYE TGGNTAVDQG IPNGNDGRGC
      351 TSEGVIHGHS GLHLFTIGTC GQVGPDVDVY EFPSEYELLL GFMLFFQRYA
20     401 PAFVTGYNIN SFDLKYILTR LEYLYKVDSQ RFCKLPTAQG GRFFLHSPAV
      451 GFKRQYAAAF PSASHNNPAS TAATKVYIAG SVVIDMYPVC MAKTNSPNYK
      501 LNTMAELYLR QRKDDLSYKD IPRCFVANAE GRAQVGRYCL QDAVLVRDLF
25     551 NTINFHYEAG AIARLAKIPL RRVIFDGQOI RIYTSLLDEC ACRDFILPNH
      601 YSKGTTVPET NSVAVSPNAA IISTAAVPGD AGSVAAMFQM SPPLQSAPSS
30     651 QDGVSPGSGS NSSSSVGVFS VSGSGSGGVG VSNDNHGAGG TAAVSYQGAT
      701 VFEPEVGYYN DPVAVFDFAS LYPSEIMAHN LCYSTLLVPG GEYPVDPADV
      751 YSVTLENGVT HRFVVRASVRV SVLSELLNKW VSQRRVREC MRECQDPVRR
35     801 MLLDKEQMAL KVTCAFYGF TGVVNGMMPC LPIAASITRI GRDMLERTAR
      851 FIKDNFSEPC FLHNFFNQED YVVGTRREGDS EESSALPEGL ETSSGGSNER
40     901 RVEARVIYGD TDSVFVRFRG LTPQALVARG PSLAHYVTAC LFVEPVKLEF
      951 EKVFSVSLMMI CKKRYIGKVE GASGLSMKGV DLVRKTACEF VKGVTRDVLS
45    1001 LLFEDREVSE AAVRLSRLSL DEVKKYGVPR GFWRLRRLV QARDDLYLHR
      1051 VRVEDLVLS VLSKDISLYR QSNLPHIAVI KRLAARSEEL PSVGDRVFYV
      1101 LTAPGVRTAP QGSSDNGDSV TAGVVSRSDA IDGTDDDADG GGVEESNRRG
50    1151 GEPAKKRARK PPSAVCNIEV AEDPSYVREH GVPIHADKYF EQVLKAVTNV
      1201 LSPVFPGET ARKDKFLHMV LPRRLHLEPA FLPYSVKAHE CC*
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